Shears, Beverly

From:

Devi, Sarvamangala

Sent:

Wednesday, July 27, 2005 3:59 PM

To:

Shears, Beverly

Subject:

10/070,882

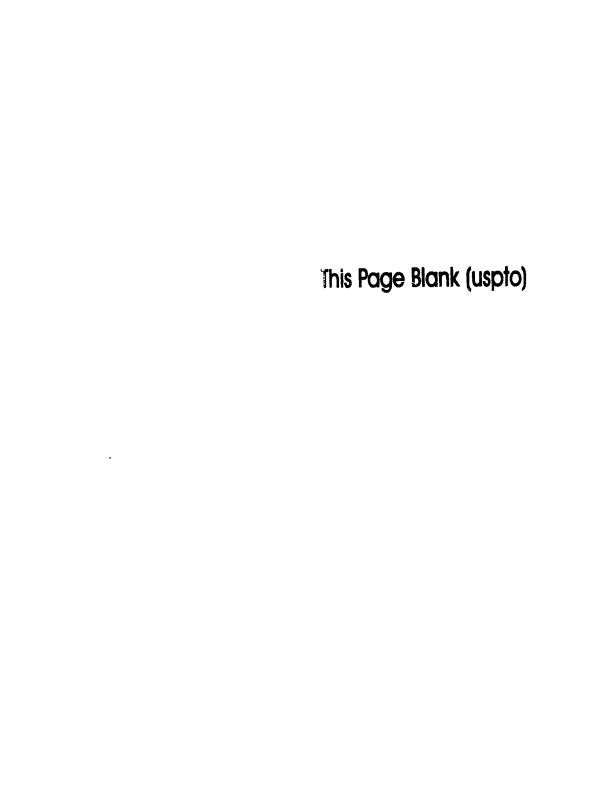
Beverly:

In application 10/070,882, please perform a sequence search for SEQ ID NO: 2 in commercial and pending databases.

Thanx.

S. DEVI, Ph.D. Primary Examiner AU 1645 Rems - 3C18

Date completed: Search Site **Vendors** Searcher: STIC Terminal time: CM-1 STN Elapsed time: Pre-S _ Dialog CPU time:_ Type of Search APS Total time: _ __ N.A. Sequence Geninfo Number of Searches: A.A. Sequence SDC Number of Databases: Structure DARC/Questel Bibliographic Other CGN PTO-1590 (9-90)





STIC Search Report Biotech-Chem Library

STIC Deteloase Translating Name

TO: Sarvamangala Devi

Art Unit: 1645

Location: REM 3C18

Serial Number: 10/070882

Tuesday, August 09, 2005

From: Beverly Shears

Location: Biotech-Chem Library

REM 1A54

Phone: 571-272-2528

beverly.shears@uspto.gov

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ALIGNMENTS

JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL REFERENCE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS REFERENCE AUTHORS TITLE PUBMED REFERENCE SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 1 AK082454/c LOCUS DEFINITION JOURNAL MEDLINE AUTHORS TITLE TITLE AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000) AKO82454

MUS musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230052F14 product:unclassifiable, full Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999) FANTOM Consortium. Functional annotat Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Mus musculus HTC; CAP trapper. The FANTOM Consortium and the Nature 409, The RIKEN Genome Exploration Research Group Phase II Team and the Mus musculus (house mouse) AK082454.1 GI:26100683 11076861 20530913 insert sequence. 11042159 annotation of a 685-690 (2001) full-length RIKEN Genome Exploration Research CDNA collection genes

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All Nature 420, 563-573 (2002)

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Adachi,J., Alzawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Adachi,J., Alzawa,K., Haramoto,K., Hiraoka,T., Hirozane,T., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Kimozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Myazaki,A., Murata,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Sano,H., Sasito,R., Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasai,D., Shibata,K., Sahaaj,K., Sakazume,N., Sano,H., Sasai,D., Shibata,K., Takaka-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Takahashi,F., Takak-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramateu,M. and Hayashizaki,Y.
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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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BY642267 RIKEN full-length enriched, vii
CDNA Clone K430350A22 3', mRNA sequence
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Please visit our web site for further details.
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Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Alizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki, Direct Submission
Computational Analysis of Full-Length Mouse cDNas Compared with
Human Genome Sequence Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNas to
prepare full-length cDNa libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Nature 420, 563-573 (2002)
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                                                                                                                                                                                                                                                                          Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a encyclopedia: real-time sequence clustering for construction of a cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                        prepare mouse tissues.
Tissues were provided by Michela Fagiolini and Takao K. Hensch (
Tissues were provided by Michela Fagiolini and Takao K. Hensch (
Tishoratory for Neuronal Circuit Development Brain Science Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 81-45-503-9222
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assistance we gratefully acknowledge. Please visit our web site (http://ge
                                                                                                RIKEN 2-1 Hirosawa, Wako-shi, Saitama 351-0198 Japan ) whose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 81-45-503-9216
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Rodentia;
              site (http://genome.gsc.riken.go.jp)
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Sciurognathi; Muridae; Murinae; Mus.
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COMMENT

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RESULT 3
AV231406
LOCUS
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AUTHORS
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FEATURES
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18 (Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Skonno, H., Aizawa, K., Akahira, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Shibata, Y., Shigemoto, Y., Shiraki, T., Tateno, M., Tominaga, N., Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Towonda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., RIKEN Mouse ESTs (Konno, H., et al. 1999)

11 Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 CTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV231406 204 bp mRNA linear AV231406 RIKEN full-length enriched, 0 day neonat musculus cDNA clone 4632406L08 3', mRNA sequence.
AV231406
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303.
                                                                                                                                                                                                                             Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
                                                                                                                                                                                                                                                                                                                                                                   Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
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Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 81-45-503-9216
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                                                                                                                                                                                                            and Hayashizaki,Y.
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/tissue_type="visual cortex"
/clone_lib="RIKEN full-length enriched, visual
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/mol_type="mRNA"
/strain="C57BL/6J"
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Location/Qualifiers
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Pred. No. 12;
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d, 0 day neonate
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REFERENCE
AUTHORS
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SOURCE
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                                                                                                           Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishi, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB775700 RIKEN full-length enriched, RCB-0559 K-1
BB775700 RIKEN full-length enriched, RCB-0559 K-1
musculus cDNA clone G430026L09 3', mRNA sequence-
BB775700
Laboratory for Genome Exploration Research Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Rese
                                                        Unpublished (2001)
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4632406L08"
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'lab_host="DH108"
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Pred. No. 18;
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    Research (RIKEN)
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SOURCE
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
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Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
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1 (bases 1 to 318)

Konno, H., Alzawa, K., Akahira, S., Pukunishi, Y., Hara, A., Hayatsu, N., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Izawa, M., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 bp mRNA linear EST 2. BB094276 RIKEN full-length enriched, 12 days embryo, embry between diaphragm region and neck Mus musculus cDNA clone 9430045021 3', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
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/clone="G430026L09"
/cell_line="RCB-0559 K-1.fl"
/clone_lib="RIKEN full-length enriched, RCB-0559
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/mol_type="mRNA"
/strain="DDD"
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Pred. No. 19;
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Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
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High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jan
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Tel: 81-45-503-9222
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                                                                                   ATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTA 134
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TTCTTCAGGACACCCCACACATTGCTTGACAGTCCTTGTTGTCA 225
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/lab host="DHIOB"
/lab host="DHIOB"
/clone lib="RIKEN full-length enriched, 12 days embryo,
/clone lib="RIKEN full-length enriched, 12 days embryo,
/clone lib="RIKEN full-length enriched, 12 days embryo,
embryonic body between diaphragm region and neck"
/note="Site 1: Sall; Site 2: BamHI; cDNA library was
/note="Site 1: Sall; Site 2: BamHI; cDNA library was
/note="Site 1: Sall; Site 2: BamHI; cDNA library
/note="Site 1: Sall; Site 2: BamHI; cDNA 
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Hirozane, T., Hori, F., Ishii, Y., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C.,
Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.
Okazaki, Y., Ono, T., Owa, C., Saito, H., Shipata, K., Shibata, Y., Shipemoto, Y., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A.,
Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A.,
Yokota, T., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A.,
Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and
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Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehito-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9216
Pax: 81-45-503-9216
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BB222962 RIKEN full-length enriched, adult male aorta and vein Mus musculus cDNA clone A530080D21 3', mRNA sequence.
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Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
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                                         prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round for formalization to the contraction of the contra
                                                                                                                                                                                                                                                       /note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
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                                                                                                                                                                           PUBMED
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RS Okazaki, Y., Puruno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Schonbach, C., Gojobori, T., Baldarelli, R., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusto, V., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusto, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Garibooldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kucohkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Malteais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Malteais, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Yang, L., Wang, Z., Zavolan, M., Zhu, Y., Zimmer, A., Yangisawa, M., Yang, I., Hara, A., Hashizume, N., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Shinadawa, T., Wayatski, A., Sakai, K., Sasaki, D., Shibata, K., Analyasi, G., Francinche, Francinche, Based on functional annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY439440 RIKEN full-length enriched,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY439440
BY439440.1
Laboratory for Genome Exploration Research Group, RIKEN Genomic, Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jag Tel: 81-45-503-9222
                                                                                                                                                                                                                                    Rogers,J., Birney,E. and Hayasnızak....
Analyais of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY439440 RIKEN full-length enriched, pooled tissues, 16 days embryo, etc. Mus musculus cDNA clone I920162D12 3', mRNA sequence.
                                                                                                                                                                                                                              Nature 420,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                           Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                      22354683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCTTCAGGACACCCCACACATTGCTTGACATTCCTTGTTGTCA
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57.7%;
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Pred. No. 20;
0; Mismatches
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                                   230-0045, Japan
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Email: genome-res@gsc.riken.jp,

URL:http://genome.gsc.riken.jp/

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RESULT 8
AZ435636/c
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                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                 VERSION
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Best Local Similarity
Matches 54; Conser
                                                                                                                                                                                                                                                             ORGANISM
TITLE
                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 157-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107
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                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 570)
1 (Dases 1 to 570)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                               AZ435636.1 GI:10559649
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ435636 570 bp DNA linear GSS 03-OCT-20
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                                                                                                                                                                                                                                                                                                Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                AZ435636
                                                                                                                                                                                                                                                                                                                                                                                                                           clone UUGC1M0222H14 R, genomic survey sequence.
Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATCAACGCTAGACTGTTCTTATTGTTA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTTCTGAGCTGTCGGTCCCACTGTTCAGATCTCTTCACTGTTTTTCTTCAGAGCACCCC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCAT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACACATTGCTTGACAGTCCTTGTTGTCA 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="pooled tissues: (dev_stage=16 days embryo,tissue_type=heart.sex=mix), (dev_stage=16 days embryo,tissue_type=kidney.sex=mix), (dev_stage=17 days embryo,tissue_type=heart.sex=mix), (dev_stage=17 days embryo,tissue_type=stomach.sex=mix), (dev_stage=17 days embryo,tissue_type=kidney.sex=mix), (dev_stage=17 days embryo,tissue_type=kidney.sex=mix), (dev_stage=17 days pregnant, adult,tissue_type=amnion,sex=female), (dev_stage=13 days_embryo,tissue_type=liver.sex=mix)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 days embryo, etc."
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/mol_type="mRNA"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="1920162D12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33.6;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS 03-OCT-2000
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VERSION
KEYWORDS
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BE131381
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                                                                                                                                                                                                                                                          DEFINITION
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Best Local
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                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                156
                                                                                                                                                                                                                             BE131381
L48-1355T3 Ice |
NaCl treatment |
                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Caryophyllales; Aizoaceae; Mesembryanthemum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 570.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0222 row: H column: 14
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: plasmid ends
                                                                                                                                                           BE131381.1
                                                                                                                                                                                                                                                                                                                                                                                                                GAGAATGTTTGTTTCCCTTA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGACTATTTGTCTGGTTTA 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGACTTTAGTCAAGCTAATTAATTTCTCCAATTCTCATCGTCTTTACTTATAAAACAGG 157
                                                                                                                                                                                                     sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                           GI:8578744
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                                                                                                                                                                                                                             590 bp mRNA linear EST 20-FEB-2001 plant Lambda Uni-Zap XR expression library, 48 hours Mesembryanthemum crystallinum cDNA clone L48-1355,
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Pred. No. 22;
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VERSION
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BM658097
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Best Local Similarity
Matches 54; Conserv
                                                                                                                        JOURNAL
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Seq primer: T3
High quality se
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Unpublished (1997)
Contact: Cushman JC
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                                                                                                                                                                                                            Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Eukaryota; Embryophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Caryophyllales; Aizoaceae; Mesembryanthemum.
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BACKWARD: T3
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Tel: 775-784-1918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCR PRimers
                 MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
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                                                                    Department of Biochemistry University of Nevada
                                                                                                         Contact: Cushman JC
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Unpublished (1997)
                                                                                                                                        An expressed sequence tag database Mesembryanthemum crystallinum
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jcushman@unr.edu
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/dev_stage="Six week old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 48 hours NaCl treatment"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
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|mal_type="mRNA"
|db_xref="taxon:3544"
|clone="148-1355"
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Pred. No. 22;
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eudicots;
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CA835622
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Best Local Similarity
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BACKWARD: T7 21mer
Plate: 059 row: H co
Seq primer: T3 20mer
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MCS039B06 160752 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM). Mesembryanthemum crystallinum cDNA clone MCS039B06 5, mRNA
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Mesembryanthemum crystallinum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Aizoaceae; Mesembryanthemum.
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Seg primer: T3 20mer
High quality sequence stop: 625.
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CA835622
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                                                                                                                                                                                                                                               Email: jcushman@unr.edu
                                                                                                                                                                                                                                                                      Fax: 775-784-1650
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775-784-1918
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/clone_lib="Ice plant Lambda Uni-Zap XR expression
/clone_lib="Ice plant Lambda Uni-Zap XR expression
/library, 48 hours NaCl treatment prescreened for removal
of highly abundant transcripts"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
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|mol_type="mRNA"
/db_xrefe"taxon:3544"
/clone="MCR059H01"
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/organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCS039B06"
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                                                                                                    Location/Qualifiers
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Pred. No. 22;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Biochemistry University of Nevada MS200, Reno, NV 89557-0014, Tel: 775-784-1918
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Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Alzoaceae; Mesembryanthemum.
1 (bases 1 to 633)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
Contact: Cushman JC
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Seq primer: T3 20mer
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BACKWARD: T7 21mer
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                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 633
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 jcushman@unr.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="leaf"
/dev gtage="five-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean
metabolism, phase I (2 AM)."
/clone_lib="Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase I (2 AM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-, Site 1: EcoRI; Site_2: XhoI, Library construction was performed according to Strategene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: ECORI; Site 2: Xhol; Library construction was performed according to Strategene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."
                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:3544"
/clone="MCS028H02"
                                                                                                                                                                        /tissue_type="leaf"
/dev_stage="five-week-old"
                                                                                                                                                                                                                                                                                           organism="Mesembryanthemum crystallinum"
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Pred. No. 22;
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BM301497
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Best Local S
Matches 54
                                                                                                                                                  Query Match
Best Local Similarity
Matches 54; Conserv
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                                  104
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                                                                                                              44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An expressed sequence tag database for the common ice plant, Mesembryanthemum crystallinum Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mesembryanthemum crystallinum Eukaryota; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Caryophyllales; Aizoaceae; Mesembryanthemum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BM301497 674 bp mRNA linear EST 22-JAN-2002 MCR046F12 26036 Ice plant Lambda Uni-Zap XR expression library, 48 hours NaCl treatment prescreened for removal of highly abundant transcripts Mesembryanthemum crystallinum cDNA clone MCR046F12 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
BM301497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: 046 row: F (
Seq primer: T3 20mer
High quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Biochemistry University of Nevada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Cushman JC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BM301497.1 GI:18023872
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BACKWARD: T7 21mer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: jcushman@unr.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 775-784-1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mesembryanthemum crystallinum (common iceplant)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
CTGAAAAAACAGTGGGAGTTTGTTTTTG 243
                            CATAATCAACGCTAGACTGTTCTTATTG 131
                                                                          TITTCATCACAAAGCAGGTGACTTTGGGTTGAAATTCTTATCCCCTAATCAACAAATCAC 215
                                                                                                      TTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCAC 103
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                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                            /organism="Mesembryanthemum crystallinum"
/mol_type="mtNA"
/db_xref="taxon:3544"
/clone="MCR046F12"
/tissue_type="leaf"
/tissue_type="leaf"
/dev_stage="six-week-old"
/clone_lib="Ice_plant Lambda Uni-Zap XR expression
/clone_lib="Ice_plant Lambda Uni-Zap XR expression
/fibrary, 48 hours NaCl treatment prescreened for remov
of highly abundant transcripts"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_Ecori; Site_2: XhoI"
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61.4%;
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Pred. No. 23;
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Pred. No. 22;
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AUTHORS
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BM301422
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                                                                                                                                    RESULT 15
CR303205
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Best Local Similarity
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 ORGANISM
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Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Alzoaceae; Mesembryanthemum.
1 [bases 1 to 699]
                                truncatula,
CR303205
CR303205.1
GSS.
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BM301422
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MCR045F12 25886 Ice plant Lambda Uni-Zap XR expression library, 48 hours NaCl treatment prescreened for removal of highly abundant transcripts Mesembryanthemum crystallinum cDNA clone MCR045F12 5,
                                                                 746 bp DN Medicago truncatula BAC ends cultivar truncatula, genomic survey sequence. CR303205
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BACKWARD: T7 21mer
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Tel: 775-784-1918
Fax: 775-784-1650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Biochemistry University of Nevada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Cushman JC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mesembryanthemum outpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   An expressed sequence tag database Mesembryanthemum crystallinum
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Medicago truncatula
                  Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                              CATAATCAACGCTAGACTGTTCTTATTG 131
                                                                                                                                                                                                                                                                                                               TTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCCAAAGCAC 103
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="six-week-old"
/clone_lib="Ice plant Lambda Uni-Zap XR expression
/library, 48 hours NaCl treatment prescreened for removal
of highly abundant transcripts"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mesembryanthemum crystallinum"
/mol_type="mRNA"
/db_xref="taxon:3544"
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                                                  GI:44708225
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Pred. No. 23;
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                                                                                                                         DNA
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                                                                                                     Jemalong
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                                                                                                       linear
long A17
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                                                                                                       GSS 28-FEB-2004
of Medicago
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AUTHORS
TITLE
Search completed: August
Job time : 7078 secs
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                                                              577
                                                                                                                              517
                                                                                              110 CAACGCTAGACTGTTCTTATTGTTAACA 137
                                                                                                                                                              50
                                                                                                                                                                                              54;
                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (25-FBB-2004) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; spermatophyta; Magnoliophyta; Eddicat; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope.
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                                                                                                                            TGATTAAGAGAGTGATGATTAGTCAATTACATACAATATATCCCCAAAAGGAGCACCAT 576
                                                               CAATGATATACTATATCCAAAATGAACA
                                                                                                                                                              TCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCCAAAGCACCATAAT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 746)
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                              mte1-21P8FM1"
                                                                                                                                                                                                                                                                                                                                      /organism="Medicago truncatula"
/mol_type="genomic DNA"
/cultivar="Jemalong A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                            clone_lib="MTE1"
                                                                                                                                                                                                             24.2%;
               4, 2005, 01:47:13
                                                                                                                                                                                               0
                                                                                                                                                                                                             Score 33.6;
Pred. No. 23;
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Scoring table:
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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                        N_Geneseq_16Dec04:*
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geneseqn2003cs:*
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    2005, 20:47:40; Search time 276 Seconds
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Compugen Ltd.
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score and is Pred. No. 18 greater than derived is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.

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	21.7	21.9	21.9	21.9	21.9	21.9	22.0	22.0	22.0	22.2	22.2	22.2	22.3	22.3	23.5	26.8	28.8	100.0	100.0	Query Match
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	ADB12064_03	ABD33157	ABQ99653	ADN48950	ACC69145	AAD63515	AAH68533	AAH67957	ACA02032	ADA57769	ADA41637	AAK81193	ABQ72685	ABQ72598	ADE87477	ACA49482	ABL57265	ADG31136	AAF82356	ID
	Concinuation (4 or	Abd33157 Murine ca	Abq99653 Human MS4	Adn48950 Mycoplasm	Acc69145 M. genita	Aad63515 Mycoplasm	Aah68533 C glutami	Aah67957 C glutami	Aca02032 C. glutam	Ada57769 BAC fragm	Ada41637 Human sec	Aak81193 Human imm	Human	Abq72598 Human MDD	Ade87477 Fowlpox v	Aca49482 Prokaryot	Abl57265 Escherich	Adg31136 Salmonell	Aaf82356 Salmonell	Description

The present sequence is a DNA fragment comprising the phop gene promoter. DNA fragments comprising the Salmonella traphimurium phop, pagC and ompC gene promoters were integrated into a vector used to transform a recombinant gut-colonising microorganism. The promoter was operably

Claim 1; Fig 6; 33pp; English.

response against pathogen.

New recombinant gut-colonizing microorganism, useful as vaccine component, comprises construct containing phoP, pagC or ompC gene promoter linked to nucleic acid encoding protein that induces immune

WPI; 2001-328017/34.

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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
29.8	29.8	29.8	29.8	29.8	29.8	29.8	29.8	29.8	29.8	29.8	29.8	29.8	29.8		29.8	•	•	29.8	29.8	29.8	29.8	29.8	30	30
21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.6	21.6
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ADB63189	ADP64619	ABL28364	ABS57323	AAZ42062	AAZ33468	ADC92238	ABL65652	ABL64736	ADS71943	ADS71710	ABV37417	ABV07484	ADG26159	ADB13743	ACC95270	ABL95106	ACA59543	AAH84956	AAH02707	AAS63734	AAH93642	AAA06526	AAK74790	ADJ38283
Adb63189 Human cDN	Adp64619 DNA of nu	Abl28364 Drosophil			Aaz33468 Human pro	Adc92238 E. faeciu	Abl65652 Lung canc	Abl64736 Lung canc	Ads71943 Human kid				Adg26159 Human pro	Adb13743 Human pro	Acc95270 Prostate			Aah84956 Human pro	Aah02707 Prostate	Aas63734 Human pro	Human	Human		Adj38283 Plastid d

ALIGNMENTS

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RESULT 1
AAF82356
ID AAF8
Salmonella typhimurium; phoP gene promoter; PphoP; antibacterial; antiviral; vaccine; lacZ; pagC; outer membrane porin C; ompC; transgenic microorganism; antigen production; antigen delivery;
                                                                                                                                                                                                                                 Salmonella typhimurium.
                                                                                                                                                                                                                                                                                             Salmonella typhimurium phoP gene promoter.
                                                                                                                                                                                                                                                                                                                               AAF82356;
                                                                                                                                                                                                                                                                                                                                               AAF82356 standard; DNA; 139
                                                                                                                                                    10-SEP-1999; 99GB-00021275.
12-JUL-2000; 2000GB-00017000.
                                                                                                                                                                             06-SEP-2000; 2000WO-GB003402.
                                                                                                                                                                                                22-MAR-2001.
                                                                                                                                                                                                                                                                                                              22-JUN-2001 (first entry)
                                                                                                                    Titball RW,
                                                                                                                                                                                                                 WO200119974-A2
                                                                                                                                                                                                                                                  infection;
                                                                                                                                    (MINA ) UK SEC FOR DEFENCE.
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                                                                                                                    Bullifent HL;
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RESULT 2
ADG31136
ID ADG3
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 139 BP; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        responses which provide protection against pathogens which colonise different host cell compartments. The Salmonella vaccine vector system is ideally suited to the delivery of many vaccine antigens since the vaccine delivery mechanism accurately mimics the natural disease, entering the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cross protective PphoPQ; promoter:
                                                                                             species, useful as a vaccine against infections caused by
                                                                                                                           New live attenuated derivative of a pathogenic Enterobacteriaceae species, useful as a vaccine for inducing cross protective immuni
                                                                                                                                                                                                                        WPI; 2004-042484/04.
P-PSDB; ADG31137, ADG31138, ADG31139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              live attenuated derivative; pathogenic Enterobacteriaceae; cross protective immunity; antibacterial; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella typhimurium PphoPQ and phoPQ operon DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADG31136 standard; DNA; 2802
Example 17; Fig 28; 133pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-APR-2002; 2002US-0372616P
18-APR-2002; 2002US-0373626P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-APR-2003; 2003WO-US011802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003096812-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                       UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rotective immunity; antibacterial; promoter; phoPQ operon; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTTCTTATTGTTAACACA 139
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Pred. No. 6.3e-36;
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RESULT 3
ABI-57265
ID ABI-5
XX ABI-5
XX ABI-5
XX ABI-5
XX Tran
XX Esch
XX II-0
FT misc
FT T T T Com
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel live attenuated derivative of a pathogenic Enterobacteriaceae species having enhanced ability to induce cross protective immunity against Enterobacteriaceae. The derivative of the invention demonstrates antibacterial and immunostimulant activities and may be useful as a vaccine for inducing a high level immune response and/or cross protective immune response to protect individuals from infection from a diversity of species or serotypes of bacterial pathogens. The current sequence is that of the Salmonella typhimurium PphoPQ and phoPQ operon DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription terminator; trpA; attenuation; vaccine; virucide; antibacterial; fungicide; antiparasitic; protozoacide; phoA; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli DNA 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL57265 standard;
                                                                                                                                                                                      (UNIW )
(MEGA-)
(CURT/)
(TING/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
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                                                                                WPI; 2002-444150/47.
                                                                                                                                    Curtiss
                                                                                                                                                                                                                                                                                                                          12-OCT-2000; 2000US-00689123
                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2001; 2001WO-US031606
                                                                                                                                                                                                                                                                                                                                                                                                                                18-APR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200230457-A2
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                                                                                                                                                                                      UNIV WASHINGTON.

MEGAN HEALTH INC
CURTISS R.

TINGE S A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCCAAAGCACCATAATCAACGCTAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2802 BP; 721 A; 702 C; 724 G; 655 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTTCTTATTGTTAACACA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTTCTTATTGTTAACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                              Tinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= b
/note= "5' overhang on complementary strand of 4 bases
with sequence 5'-GATC-3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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ຊື່ອ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single-stranded overhang"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phoA coding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 139; DB 12;
Pred. No. 1.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Composition comprising microbe having attenuating mutation that comprises insertion sequence containing recombinant transcription terminator,

useful as vaccine, and for delivering a desired gene product to

Example 5; Fig 11; 91pp; English.

individual

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RESULT 4
ACA49482
ID ACA49482
ACA 49482
AC ACA4
AC ACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cc sequence of Escherichia coli. The sequence was used to illustrate an example of the invention relating to deletion of the phoA gene and replacement with a trpA terminator. The phoA mutation was introduced into Salmonella typhimurium SI1344 to produce strain MGN-1362. The present invention is based on the discovery that transcription terminators (TTs) can be inserted in a bacterial gene in an attenuating strategy which not only attenuates the virulence of the bacteria, but also serves to restrict the effect of the attenuating mutation to the target gene or operon of the bacteria. A claimed vaccine comprises a microorganism comprising an attenuating mutation in a chromosomal gene, the mutation comprising an insertion sequence which contains a recombinant TT, such as trpA. The microorganism is preferably salmonella, Shigella or trpA. The microorganism is preferably inserted in the phop gene. The Secherichia, and the TT is preferably inserted in the phop gene. The croduct from a virus, bacterium, protozoan, parasite or fungus, or can desired gene microorganism is also used in a claimed method for delivering is also used in a claimed method for delivering to a desired gene.
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Best Local !
                                                                                                                                                                     Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                      21-MAR-2001; 2001US-00815242.

06-SEP-2001; 2001US-00948993.

25-CCT-2001; 2001US-034292P.

08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 41 BP; 10 A; 13 C; 4 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUN-2003
  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella paratyphi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antisense; ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prokaryotic essential gene #31139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACA49482 standard; DNA; 1385
                                                                                  P-PSDB;
                                                                                                                                                                                                                                                           (ELIT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  design;
                                                                                                                2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 TCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTT
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                                                                                     ABU45612.
                                                                                                                                                                                                                                                           ELITRA PHARM
                                                                                                                                                                     Zamudio
Trawick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene product to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                    2002US-0362699P
                                                                                                                                                                   g,c
                                                                                                                                                                     Malone (
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                                                                                                                                                                                                                                                              INC.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of DNA located 5' to the phoA coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВÞ
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                                                                                                                                                                     Haselbeck R, Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB
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                                                                                                                                                                     Ohlsen KL,
Forsyth RA,
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                                                                                                                                                                           Zyskind JW
Xu HH;
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isolate candidate molecules for rational drug
   discovery programs
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Claim 14; SEQ ID NO 37352; 1766pp; English.

(1) a vector comprising a promoter operably linked to the nucleic acid concoding a polypeptide whose expression is inhibited by the antisense concleic acid; (2) a host cell containing the vector; (3) an isolated content of the nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense content of the polypeptide; (5) producing the polypeptide; (6) inhibited by the content of the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that inhibits cellular proliferation; (8) content of the proliferation, or that inhibits cellular proliferation of the product lies or a gene on which the test compound that inhibits proliferation of an compound that inhibits proliferation of an compound that content of an compound that inhibits proliferation of an compound that inhibits proliferation of an content of the programs, or for screening bomologous nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation in cells other than S. aureus, S. typhimurium, crequired for proliferation in cells other than S. aureus, S. typhimurium, crequired for proliferation of cells other than S. aureus, S. typhimurium, crequired for content directly from WIPO at the content of the printed specification, but was obtained in cells content of the printed specification, but was obtained in cells content of the printed specification, but was obtained in cells content of the printed specification. the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression ftp.wipo.int/pub/published_pct_sequences

Query Match Matches Best Local Sequence 1385 BP; 1344 GTGACTCTGGTCGACGAACTTAAATAATATGTGCCTCACCCT 1385 1 GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCT 42 Similarity Conservative 353 A; 372 C; 335 G; 321 T; 0 U; 4 Other; 26.8%; ٥. Score Pred. Mismatches a 37.2; had no 0.054; 8, u T Length 1385; Indels 0; Gaps 0

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fowlpox virus; FPV; virucide; tuberculostatic; protozoacide; cytostatic; hepatotropic; antibacterial; vaccine; malaria; tubest Coast fever; avipox virus; influenza; hepatitis;
30-NOV-2001; 2001GB-00028733: 30-NOV-2001; 2001US-0334649P.
                                                                                                                  gene;
                                                                                                                                                                               Fowlpox virus
                                                                                                                                                                                                      29-JAN-2004 (first entry)
                                                                                                                                                                                                                                               ADE87477 standard; DNA; 266145 BP
                               02-DEC-2002; 2002WO-GB005411
                                                                                             Fowlpox virus.
                                                                                                                                                                                                                           ADE87477;
                                                                        WO2003047617-A2
                                                                                                                 papilloma virus; tumour; ds.
                                                                                                                                                                               genome
                                                                                                                                                                                  DNA.
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tuberculosis;

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ABQ72598/c
ID ABQ725
XX
AC ABQ725
XX
DT 03-SEP
DX 03-SEP
DX Human |
XX
Human |
XX
Human |
XX
Frequency
XX
Homo si
XX
PD 23-MAY
PD 23-MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC modifications in one or more wild-type FPV genes. The invention further CC modifications in one or more wild-type FPV genes. The invention further CC relates to a novel method for treating and/or preventing a disease in a CC subject comprising administering two compositions, each containing a non-CC replicating viral vector. At least one of the compositions comprises a CC poxvirus vector derived from a fowlpox virus. The novel compositions have CC the following activities: virucide, tuberculostatic, protozoacide, CC antipyretic, cytostatic, hepatotropic, and antibacterial. The non-CC particularly a mammal such as a primate, specifically human. The priming CC or boosting composition, or the kit is useful for manufacturing a CC medicament for treating and/or preventing a disease which is, or results CC from, a chronic infection such as malaria, tuberculosis or East Coast CC fever, or for eliciting a T-cell immune response in a subject. Non-CC cultured CEF cells are useful for growing an avipox virus, such as CC fowlpox virus. The method or the vaccine may further be used to treat or prevent influenza, hepatitis, human papilloma virus and other viral CC infections, malignancies such as tumours, leishmaniasis, listeriosis, and CC virus genome of the invention.
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Best Local S
Matches 62
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                                                                                                                     Human; MDDT; disease detection and treatment molecule polynucleotide; proliferative disorder; hepatitis; psoriasis; cancer; AIDS; autoimmune disorder; inflammatory disorder; allergy; multiple sclerosis; rheumatoid arthritis; transgenic; gene therapy; antiarteriosclerotic; hepatotropic; antiinflammatory; antipsoriatic; cytostatic; anti-HIV; antiallergic; antianaemic; antiasthmatic; antiatherosclerotic; antigout;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 266145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ISIS-)
                                                                                                                                                                                                                                                                                                                                                        ABQ72598 standard;
                                                                                                        neuroprotective;
                                                                                                                                                                                                                                                                                  03-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                         σ
                                                                                                                                                                                                                                                                                                                                                                                                                                              21241 TTATGATGTTTCTGTCCATAAAGGGTAATGATCAATACTATAATGTTTTTA 21291
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                                                                     sapiens.
                                                                                                                                                                                                                                                 MDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTATTAACTGTTTATCCCCAAAAGCACCATAATCAACGCTAGACTGTTCTTA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGTTACTTATAGATATATTTAATATCTTATCGACGGAAGGACGAAGATCCATGGTATGTG
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                                                                                                                                                                                                                                              encoding
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                                                                                                        antirheumatic; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                        cDNA;
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Pred. No. 8
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2000US-0230951P.
2000US-0231163P.
2000US-0231167P.
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2000US-0230518P

2000US-0230519P

2000US-0230597P

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2000US-0230659P

2000US-0230619P

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2000US-0229749P.
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2000US-0230583P.
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Jackson S, Hillman JL, Dahl CR, Mc Hillman JL, Jones AL, Dahl CR, Momiyama MG, Roseberry AM, Gerstin Daffo A, Marwaha R, C Lincoln SE, E, Altus CM, Dufour GE, Chalup MS;
Yu JY, Wright RJ, Gletzen D, Liu
, Bradley DL, Rohatgi SD, Harris B;
n EH, Peralta CH, David MH, Panzer S
Chen AJ, Chang SC, Au AP, Inman RR; Liu TF, SR, Yap

2002-527544/56

Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders e.g. arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder e.g ė

Claim 1; Page 390-391; 618pp; English.

compound for effectiveness in altering expression of a target gorgening a compound for effectiveness in altering expression of a target compound for effectiveness in altering expression of a target compound, or detecting MDDT in a sample or for assessing toxicity of a test compound, in a diagnostic test for a condition or a disease associated with the composition of a tissue or condition or a disease associated with the composition comprising (I) in a sample, and for purifying (I) from a sample. A composition comprising (I), an associated with decreased or increased expression of functional MDDT. (I) associated with aberrant expression of MDDT, where the disorders are selected from a cell proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis, psoriasis, and cancer and an cautoimmune/inflammatory disorder such as AIDS, Addison's disease, allergy, anaemia, asthma, atherosclerosis, gout, multiple sclerosis or rheumatoid arthritis. (II) are useful for creating knockin humanised canimals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to The invention relates to an isolated human disease detection and treatment (MDDT) polypeptide (I) selected from a polypeptide having a sequence selected from 254 sequences (ABP51231-ABP51484) given in the specification, a naturally occurring polypeptide comprising a sequence having at least 90% identity to (I) or a biologically active or immunogenic fragment of (I). (I) is useful for screening a compound for effectiveness as an agonist or antagonist, for screening a compound the specifically binds (I) or modulates the activity of (I), and for preparing a polyclonal or monoclonal antibody by hybridoma technology. Nucleic acids (II) (ABQ72449-ABQ72700) encoding (I) are useful for

WO200240715-A2

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RESULT 7
ABQ72685/c
ID 7ABQ726
XX ABQ726
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XX Human |
XX Hu
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Best Local S
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05-SEP-2000;

05-SEP-2000;

05-SEP-2000;

05-SEP-2000;

06-SEP-2000;

06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; MDDT; disease detection and treatment molecule polynucleotide; proliferative disorder; hepatitis; psoriasis; cancer; AIDS; autoimmune disorder; inflammatory disorder; altergy; multiple sclerosis; rheumatoid arthritis; transgenic; gene therapy; antiarteriosclerotic; hepatotropic; antiinflammatory; antipsoriatic; cytostatic; anti-HIV; antiallergic; antianaemic; antiasthmatic; antiaterosclerotic; antigout; neuroprotective; antirheumatic; antiarthritic; gene; ss.
  Jackson
Hillman
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2000US-023050SP.
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2000US-023059SP.
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  Lincoln SE,
Jones AL,
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  Altus CM, Dufour GE, Chal
Yu JY, Wright RJ, Gietzen
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Daffo A,
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AM, Gerstin
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EH, Peralta CH, Da
Chen AJ, Chang SC,
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2002-527544/56.

Novel human disease detection and treatment polypeptide, useful in diagnosis, prevention or treatment of cell proliferative disorders $e\cdot g$ arteriosclerosis, cirrhosis and an autoimmune/inflammatory disorder $e\cdot g$ Ġ ò

Claim 435; 618pp; English.

The invention relates to an isolated human disease detection and CC treatment (MDDT) polypeptide [1] selected from a polypeptide having a CC sequence selected from 254 sequences (ABPS1231-ABPS1484) given in the CC sequence selected from 254 sequences (ABPS1231-ABPS1484) given in the CC specification, a naturally occurring polypeptide comprising a sequence community of [1]. (1) is useful for screening a compound for CC immunogenic fragment of [1]. (1) is useful for screening a compound that specifically binds (1) or monoclonal antibody by hybridoma technology. CC unclaic acids (11) (AB072449-AB072700) encoding (1) are useful for CC screening a compound for effectiveness in altering expression of a target CC polynucleotide comprising. Oligonucleotides and antibodies are useful for CC detecting MDDT in a sample or for assessing toxicity of a test compound, CC in a diagnostic test for a condition or a disease associated with the CC expression of MDDT in a biological sample, for detecting (1) in a sample, CC and for purifying (1) from a sample. A composition comprising (1), an CC associated with decreased or increased expression of functional MDDT. (1) associated with decreased or increased expression of functional MDDT. (1) or (II) are useful for diagnosing, treating or preventing disorders associated with aberrant expression of MDDT, where the disorders are selected from a cell proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis, psoriasis, and cancer and an autoimmune/inflammatory disorder such as AIDS, Addison's disease, allergy, anaemia, asthma, atherosclerosis, gout, multiple sclerosis or rheumatoid arthritis. (II) are useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation or inversion among normal, carrier or affected individuals and as hybridisation probes for mapping naturally occurring genomic

Sequence 810 BP; 262 A; 153 C; 165 G. 230 T; 0 U; 0 Other;

Matches Best Query Match Local 55; Similarity TTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCCAAAGCACC 104 Conservative 22.3%; <u>,</u> Score 31; DB Pred. No. 5.2; Mismatches 6, 40; Length 810; Indels <u>.</u> Gaps 0

8

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549

Ś 밁 밁 489 105 ATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139 TTCTGTAATGCTAGAAATCTCTCAGTGTCAACACA 4555

TTCCAATAAAAAAAGTCCTCCATTTAGTTTATTTTATCACAGTTTTGTCCAAAAGCGCT

490

RESULT 8 AAK81193/c

AAK81193 standard; DNA; 19521 BP

AAK81193,

07-NOV-2001 (first entry)

immune/haematopoietic antigen genomic sequence SEQ ID NO:36005.

SEXEXEXEX Human; immune; haematopoietic; immune/haematopoietic cytostatic; gene therapy; vaccine; metastasis; ds. antigen; cancer

14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 21-SEP-2000; 21-SEP-2000; 25-SEP-2000; 25-SEP-2000;	Homo sapiens WO200157182 09-AUG-2001. 17-JAN-2000; 24-FEB-2000; 16-MAR-2000; 11-MAR-2000; 11-MAR-2000; 11-MAY-2000; 28-JUN-2000; 29-JUN-2000; 10-JUL-2000; 11-JUL-2000; 11-AUG-2000; 11-A
0232398 0232398 0232400 0232400 0233063 0233063 0233064 0234223 0234223 0234223 0234223	A2. 2001W0-US001354. 2000US-01186528P. 2000US-01186528P. 2000US-011865350P. 2000US-01188135P. 2000US-0205515P. 2000US-0215135P. 2000US-0215135P. 2000US-0215135P. 2000US-0215135P. 2000US-0215135P. 2000US-0215135P. 2000US-0215139P. 2000US-0225513P. 2000US-0225513P. 2000US-0225513P. 2000US-0225514P. 2000US-0225514P. 2000US-0225514P. 2000US-0225514P. 2000US-0225514P. 2000US-0225514P. 2000US-0225514P. 2000US-0225514P. 2000US-0225514P. 2000US-0225568P. 2000US-022575P. 2000US-022575P. 2000US-022575P. 2000US-0225758P. 2000US-0225759P. 2000US-0235758P. 2000US-0235758P
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WPI; 2001-483426/52

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(HUMA-) HUMAN GENOME SCI INC

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RESULT 9
ADA41637/c
ID ADA41637;
XX ADA41637;
AC ADA41637;
AC ADA41637;
XX DT 20-NOV-20(
XX Human sec)
XX Human; sec,
XX Wound heal
XX wound heal
XX Wolnerary;
XX WO20021029
XX WO20021029
XX PD 27-DEC-20(
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PR 11-NOV-20(
XX 11-NOV-2
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activity, and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic seguences from the present invention. AAK59492 to AAK8950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19521 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                        anaemia; allergic reaction; asthma; cardiovascular disorder;
wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
                                21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              vulnerary; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; secreted protein; cancer; hyperproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-NOV-2003
                                                                                                                                                         19-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rheumatoid arthritis; autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secreted protein related DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTAACTCTGGGCAACTTACATAAACTCTCTGTGCCTCAGCTTCTGCACCTGAGAAAAGGG 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; DNA; 19521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d sequences given in AAM82170 to AAM91921.
and can be used in gene therapy and vacci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                2002WO-US008123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO 36005; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.2%;
                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and metastas:
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorder; haematopoietic
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No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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cc treating or ameliorating medical conditions e.g. by protein or gene ct therapy. The polypeptides, nucleic acid molecules, antibodies or their cc fragments, and agonists or antagonists that bind to the polypeptide are useful for preparing a diagnostic or pharmaceutical composition for cc diagnosing or treating cancer or other hyperproliferative disorder. The cc polypeptides and nucleic acid molecules are also useful for detecting, creventing, diagnosing, prognosticating, treating or ameliorating cancer or other hyperproliferative disorders including neoplasms, autoimmune cc erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic anaemia), haematopoietic or haematological disorders (e.g. anaemia, climbers) (e.g. ischaemia-reperfusion injury, inflammatory bowel disease or Crohn's disease), neurodegenerative disorders (e.g. alaheimatory bowel disease or Parkinson's disease), cardiovascular disorders (e.g. Alaheimer's disease or Parkinson's disease), cardiovascular disorders (e.g. alaheimer's disease or parkinson's disease), or wound healing and disorders of epithelial cell proliferation. The nucleic acide are also useful for chromosome identification, radiation hybrid mapping or long-craft providing immunological probes for differential identification of the tissues immunological probes for differential identification appring or servince of epithelial cell probes. The polypeptides and antibodies are useful for providing immunological probes for differential identification appring of apprinces the polypeptides and antibodies are also constituted to the providing are constituted to human secreted proteins. Note: The sequence of this patent did not form part of the proteins. Note: The sequence of this patent did not form part of the proteins are constituted to human secreted proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preventing or treating asthma, allergies or AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human secreted proteins and nucleic acid molecules, useful for preparing a diagnostic or pharmaceutical composition for diagnosing, preventing or treating cancer or other hyperprolliferative disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel genes ADA39629-ADA40565 and proteins ADA40566-ADA41501 for human secreted proteins, useful for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME
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                                                                                       Local Similarity
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                   GIGACTATTIGICT
CTAACAATTCCTAT 1238
                                       GTAACTCTGGGCAACTTACATAAACTCTCTGTGCCTCAGCTTCTGCACCTGAGAAAAGGG
                                                          GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG
                                                                              Conservative
                                                                                      22.2%;
                                                                               <u>.</u>
                                                                                         Pred. No.
                                                                                                Score 30.8;
                                                                              Mismatches
                                                                                          15;
                                                                                                   DB
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                                                                                                  Length 19521;
                                                                                Indels
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                                                                               Gaps
                                         1252
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Sequence 19521 BP;

5672 A; 3465 C; 3902 G; 6482

T; 0 U; 0 Other;

the printed

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specification, but was obtained in electronic format
tftp.wipo.int/pub/published_pct_sequences.

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cytostatīc; cerebroprotective; neuroprotective; noo
cardiovascular; antiarteriosclerotic; gene therapy;
human secreted protein; immune disorder; inflammati
respiratory disorder; cancer; CNS disorder; neurode
                                                                                                   BAC fragment
                                                                                                                                       20-NOV-2003
                                                                                                                                                                                                         ADA57769 standard;
                                                                   immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
                                                                                                   containing human secreted protein gene
                                                                                                                                     (first entry)
                                                                                                                                                                                                         DNA; 19521 BP
                     inflammation,
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neurodegenerative disorders;

nootropic,

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                                                                                                                                                                                                                                ce neurodegenerative disorders, or polypeptides comprising an amino acid sequence at least 95% identical to the new sequences. The polypeptides, antibodies or antibody fragments that bind to the polypeptides, mucleic cards encoding the polypeptides, agonists on antagonists that binds to the polypeptides, aponists or antagonists that binds to the polypeptide, are useful in preparing diagnostic or pharmaceutical compositions for diagnosing, treating or preventing an e.g. immune cities or Crohn's disease), respiratory disorders (e.g. asthma and allergy), cancers (e.g. gastric, ovarian or lung cancer), CRS disorders (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative cardiovascular disorders (e.g. atherosclerosis or myocarditis). The cardiovascular asmples, in forensic biology, and as hybridization or antisense DNA or RNA, in gene expression through triple helix formation or antisense DNA or RNA, in gene therapy, for identifying individuals cardium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) gels, to raise antibodies, for testing biology, and as hybridization composition of preventing neural disorders, immune system disorders, cardiovascular, reproductive, gastrointestinal, pulmonary, cardiovascular, cardiovascular, general artificial chromosome (BAC) fragment containing the gene encoding one of the polypeptides of the invention. Note: The sequence corresponds to a bacterial artificial chromosome (BAC) fragment containing the gene encoding one of the polypeptides of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                         Matches
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19-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy; multiple sclerosis; ischaemic brain injury; Parkinson's disease; Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping; triple helix formation; antisense gene therapy; forensic biology; ds; gene; bacterial artificial chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to 592 new human secreted polypeptides useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human secreted polypeptides and polynucleotides, useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or
                                                                                                                                                                                                                              Sequence 19521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 1962; 1754pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurodegenerative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-167512/16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAR-2002; 2002WO-US008278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-DEC-2002
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                                                                                                                                                            Local Similarity
                                                 1311
    61
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    GTGACTATTTGTCT 74
                                                 GTAACTCTGGGCAACTTACATAAACTCTCTGTGCCTCAGCTTCTGCACCTGAGAAAAGGG
                                                                                             GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG
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                                                                                                                                         Conservative
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2001US-0306171P.
2001US-0331287P.
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                                                                                                                                                            22.2%;
                                                                                                                                                               Score 30.8;
Pred. No. 1
                                                                                                                                         Mismatches
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RESULT 11
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ID ACA022
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AAH67957
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Best Local S
Matches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes a novel nucleic acid array involving Corynebacterium glutamicum polynucleotides. The arrays are used to canalyse C. glutamicum, particularly for monitoring a fermentation process to determine expression levels of C. glutamicum cellular mRNA. Such monitoring particularly differentiates between expression levels of different strains of C. glutamicum and allows the adjustment of different culture and fermentation conditions. ACA00010-ACA02188 represent C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C. glutamicum derived ORF SEQ ID
                      C glutamicum coding sequence fragment
                                                                                                                                                                                   AAH67957 standard; DNA; 2799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 665-666; 709pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid array useful for Corynebacterium glutamicum during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE10128510-A1
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                                                                             26-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1251 CTAACAATTCCTAT 1238
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                                                                                                                                                                                                                                                                                                                       ATCATCGACAGTGTCTGTTCACACCACCAAATTCACCGATCCAACGTGATGATCGGT 357
                                                                                                                                                                                                                                                                                                                                                                                                                           AACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGG 76
                                                                                                                                                                                                                                                                                                                                                                      TTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       derived polynucleotides described in the disclosure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22.0%;
llarity 53.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            393 A; 394 C; 414 G; 338 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfefferle W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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Pred. No. 8.4;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fermentation,
                              SEQ ID NO: 2992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bathe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.4;
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RESULT 13
AAH68533/c
ID AAH68
XX AAH68
AC AAH68

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Best Local Similarity
Matches 63; Conserv
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07-APR-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakagawa
Tateishi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the expression profile or expression pattern of a gene derived from Coryneform bacterium, and identifying a homologue of a gene derived from coryneform bacterium. Coryneform bacteria are useful for producing amino acids, nucleic acids, vitamins, saccharides and organic acids, and particularly L-lygine. The present sequence is a nucleic acid described in the exemplification of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of nucleotide and protein sequences from the Coryneform bacterium Corynebacterium glutamicum. These are useful for identifying the mutation point of a gene derived from a mutant of coryneform bacterium, measuring expression amount and analysing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing expression profile or pattern of a gene and identifying homologous gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corynebacterium
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                                                                                                                                                                                    C glutamicum coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2799 BP; 715 A; 731 C;
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                                                                                                                                Coryneform
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                                                                                                                                                                                                                                                                                          AAH68533;
                                                                                                                                                                                                                                                                                                                                              AAH68533 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 2992;
                                                                                                                                bacterium; amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99JP-00377484.
2000JP-00159162.
2000JP-00280988.
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Senoh A, Ikeda
                                                                                                        synthesis;
                                                                                                                                                                                                                                         (first
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                                                                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.0%;
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da M,
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Pred. No. 10;
0; Mismatches
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                                                                                                                                                                                    fragment SEQ ID NO: 7068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S, Hayashi M,
Ozaki A;
                                                                                                                                   synthesis; vitamin; saccharide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Length 2799;
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EP1108790-A2

20-SEP-2001; 2001US-00960858

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RESULT 14
AAD63515/c
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakagawa
Tateishi
                                                                                                                                                  Genetic operating system; nanomachine genome; bioreactor; bioremediation; therapeutic biomolecule; energy conversion system; processing system; anabolic; catabolic system; biological film; cosmetic application;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 349980 BP; 81250 A; 97718 C; 90621 G; 80391 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation point of a gene, measuring expression of a gene, expression profile or pattern of a gene and identifying h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel polynucleotides derived from Coryneform bacteria, for identifying mutation point of a gene, measuring expression of a gene, analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-376931/40.
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07-APR-2000;
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                                                                                                                                       coating;
                                                                                                                                                                                                              Mycoplasma genitalium gene involved
                                                                                                                                                                                                                                                12-FEB-2004
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                                                                                                        Mycoplasma genitalium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     дs
                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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2000JP-00159162
2000JP-00280988
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Senoh A, Ikeda
                                                                                                                                                                                                                                                                                                            DNA;
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53.8%;
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da M, Ozaki A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30.6;
Pred. No. 3
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RESULT 15
ACC59145/c
ID ACC691
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 31241 BP; 10733 A; 4570 C; 5361 G; 10577 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-851721/79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation; metabolism; basic genetic operating system; gene therapy; autonomous prototrophic nanomachine; auxotrophic nanomachine; nanomachine; bioreactor; bioremediation; therapeutic; delivery system; artificial tissue; artificial organ system; energy conversion system; artificial tissue; artificial organ system; energy conversion system; processing system; anabolic system; catabolic system; biological film;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACC69145 standard; DNA; 31241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma genitalium nanomachine gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M. genitalium transport and binding gene cassette DNA SEQ ID NO:13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUL-2003
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                                                                                                                                                                                                                                                                                                                                   WO2003025145-A2
                                                                                                                                                                                                                                                                                                                                                                                        Mycoplasma genitalium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma genitalium; gene cassette; replication; transcription;
                                                                                             (EGEA-) EGEA
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                                                                                             BIOSCIENCES INC
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WPI; 2003-354602/33.

Evans GA

New basic genetic operating system for autonomous prototrophic or auxotrophic nanomachine, useful for therapeutic, diagnostic or in purposes, comprises a nanomachine genome encoding a gene set for viability or replication. industrial

Example 1; Page 231-240; 250pp; English

cc autonomous prototrophic or auxotrophic nanomachine comprising a nanomachine genome encoding a minimal gene set sufficient for viability cor replication, optionally in the presence of an auxotrophic molecule. CC Also described is an autonomous prototrophic or auxotrophic molecule. CC comprising a basic genetic operating system for auxotrophic nanomachine comprising a basic genetic operating system for auxotrophic molecule, and a particle envelope. The nanomachines can be used in gene therapy. The basic genetic operating system or nanomachine cc is used in gene therapy. The basic genetic operating system or nanomachine cd a bioreactor, for bioremediation, for the production of a therapeutic diagnostic indicator or reagent, for the production of a diagnostic indicator or reagent, as a delivery system, as an artificial ctissue or organ system, as an energy conversion system, as a processing system, as an anabolic or catabolic system, for the production of subsidiation of subsidiations. The present and synthesis of a basic genetic operation system for the present considered which is used in an example from the present invention for the consideration. The present invention describes a basic genetic operating system for an replication competent nanomachine

Sequence 31241 BP; 10733 A; 4570 C; 5361 G; 10577 T; 0 U; 0 Other;

Query Match Best Local (Matches Similarity Conservative 21.9**%**; 55.8%; 0; Score 30.4; Pred. No. 23 Mismatches DB 10; 46; Length 31241; Indels 0 Gaps 0

93

á 밁 S 25866 25806 ATTAAAAGAACGCTATCAAATCTATACCCCTTTTTTTTGCTAAAA 25763 94 CCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAACA

Search completed: August Job time : 282 secs Ü 2005, 21:57:32

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Maximum Match 100%
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1: /cgn2 6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2 6/ptodata/2/pubpna/PCT NEW PUB.seq:*

3: /cgn2 6/ptodata/2/pubpna/US06 NEW PUB.seq:*

4: /cgn2 6/ptodata/2/pubpna/US06 PUBCOMB.seq:*

5: /cgn2 6/ptodata/2/pubpna/US07 NEW PUB.seq:*

6: /cgn2 6/ptodata/2/pubpna/US07 NEW PUB.seq:*

6: /cgn2 6/ptodata/2/pubpna/US08 NEW PUB.seq:*

7: /cgn2 6/ptodata/2/pubpna/US08 NEW PUB.seq:*

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10:
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/ Cgm2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq: */cgm2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq: */cgm2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq: */cgm2_6/ptodata/2/pubpna/US09_NEW_PUB.seq: */cgm2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq: */cgm2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq: */cgm2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq: */cgm2_6/ptodata/2/pub
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	5 32.6 31	C 2 33	1
22.2		23.7	nery
810 2337	266145 772 810	100596	Query Match Length DB ID
21	19	22	DB
US-10-363-829-237 US-10-486-706-223	US-10-856-118-1 US-10-363-829-150 US-10-363-829-237	US-10-737-082-92 US-10-765-790-92	DB ID
Sequence 237, App Sequence 223, App	Sequence 1, Appli Sequence 150, App	sequence 92, Appl sequence 92, Appl	Description

	us-		1400	21.4	9	, <u>4</u> ,	
Sequence 229999,	-SD		617	21.4	29.8	44	
229999	-SD		61.	21.4	29.8	43	
3989,			492	21.4	29.8	42	
307	us-		492	21.4	29.8	41	
962,		9	492	21.4	29.8	40	
Sequence 46, Appl	US-09-954-456-4		492	21.4	29.8	39	
109	US-10-027-632	3 17	46	21.4	29.8	ა 8	
Sequence 109769,	US-		463	21.4	29.8	37	
	US-10-027-632-		444	21.4	29.8	36	
81146	US-		444	21.4	29.8	ა 5	
	US-10-102-		434	21.4	29.8	34	
307,	-Sn		43	21.4	29.8	33	
374	US-10-357-930-		409	21.4	29.8	32	
7475	-Sn		340	21.4	29.8	31	
293	-Sn		301	21.4	29.8	30	
293	-Sn		301	21.4	29.8	29	
293	US-10-010-940-2		301	21.4	29.8	28	
æ	US-10-012		301	21.4	29.8	27	
293,	US-09-895-814-		301	21.4	29.8	26	
293,	US-09-895-793-29		301	21.4	.29.8	25	
293,	US-09-232-880-29		301	21.4	8	24	
	US-09-822-827-		301	21.4	8	23	
293,	US-09-780-669-		301	21.4	29.8	22	
293, 1	US-09-759		301		8	21	
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Sequence 105245,	8 US-	,	458	21.6	0	19	ი
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e 137,	9 US-10-322-28:		109559		0.4	16	Ω
e 79,	9 US-10-433-287-		104644	Ľ	0.4	15	a
Sequence 13, Appl	US-10-251-668-		31241	21.9	0.4	14	O
13,	US-09-960-85		31241	۳	0.4	13	O
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Sequence 1, Appl:	9 US-09-738-626-1	0	330940	22.0	30.6	ø	O

ALIGNMENTS

RESULT 1

US-10-282-122A-37352 ; Sequence 37352, Application US/10282122A · Publication No. US20040029128A1
; GENERAL INFORMATION: ; APPLICANT: Wang, Liangsu
••
; APPLICANT: Malone, Cheryr ; APPLICANT: Haselbeck, Robert
••
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
••
; APPLICANT: Xu, H.
Ā
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347

FILING DATE:

2000-09-09

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                                                                                                                      US-10-737-082-92
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Best Local :
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                                                                   Query Match
Best Local (
                                                                                                                                                                                      SEQ ID NO 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 92, Application US/10737082 Publication No. US20050130170A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: n=g, -10-282-122A-37352
                                                       Matches
                                                                                                                                                                                                                                                                   APPLICANT: Li, Zheng
TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
FILE REFERENCE: 1657/2032
CURRENT APPLICATION NUMBER: US/10/737,082
CURRENT FILING DATE: 2003-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 78614 SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 10/737,082 PRIOR FILING DATE: 2003-12-16 NUMBER OF SEQ ID NOS: 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bayer Healthcare LLC
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OTHER INFORMATION: n=g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEATURE: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Salmonella paratyphi A
                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                     TYPE: DNA
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OTHER INFORMATION: n=g,
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                                                                                                                                                                       LENGTH: 100596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/242,578 FILING DATE: 2000-10-23
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18 ACTTAAATAATGCCTGCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGT 77
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                                                                     Similarity
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Gannon, Allison
Harvey, Jeanne
Lechner, John F.
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                                                                                                                                                                                                                                                                                                                                                                                                                          Beard, Chris
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                                                       Conservative
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92.9%;
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Pred. No. 0.074;
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                                                    Score 33; DB 22; Length 100596; Pred. No. 12; 0; Mismatches 25; Indels 0;
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Sequence 1, Application US/10856118
Publication No. US20050025747A1
GENERAL INFORMATION:
APPLICANT: Laidlaw, Stephen
APPLICANT: Skinner, Mike
APPLICANT: Hill, Adrian V.S.
APPLICANT: Gilbert, Sarah C.
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                                                                                                                 APPLICANT: Anderson, Richard
TITLE OF INVENTION: Vaccine
FILE REFERENCE: 3742.1000-000
CURRENT APPLICATION NUMBER: US/10/856,118
CURRENT FILING DATE: 2004-05-27
PRIOR APPLICATION NUMBER: PCT/GB02/005411
PRIOR APPLICATION NUMBER: GB0128733.3
PRIOR APPLICATION NUMBER: GB0128733.3
PRIOR APPLICATION NUMBER: GB0128733.3
PRIOR APPLICATION NUMBER: GB0128733.3
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 41
                                                       SOFTWARE: FASTSEQ for
SEQ ID NO 1
LENGTH: 266145
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Best Local Similarity 65.8%;
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CURRENT APPLICATION NUMBER: US/10/765,790

CURRENT FILING DATE: 2004-01-27

PRIOR APPLICATION NUMBER: US 10/737,082

PRIOR FILING DATE: 2003-12-16

NUMBER OF SEQ ID NOS: 300
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APPLICANT: Beard, Chris
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TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 100596
TYPE: DNA
ORGANISM: Artificial Sequence FEATURE:
                                        TYPE: DNA
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Gannon, Allison
Harvey, Jeanne
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                                                                                                       Windows Version 4.0
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Pred. No. 12;
0; Mismatches
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; FEATURE:
, NAME/KBY: misc_feature
; OTHER INFORMATION: Incyte ID No:
US-10-363-829-150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Jackson, Stuart E.; Lincoin, Gerard E.;
APPLICANT: Altus, Christina M.; Dufour, Gerard E.;
APPLICANT: Chalup, Michael S.; Jackson, Jennifer L.;
APPLICANT: Jones, Anissa L.; Yu, Jimmy Y.;
APPLICANT: Wright, Rachel J.; Gietzen, Darryl;
APPLICANT: Liu, Tommy F.; Yap, Pierre E.;
APPLICANT: Liu, Christopher R.; Momiyama, Monika G.;
APPLICANT: Bradley, Diana L.; Rohatgi, Sameer D.;
APPLICANT: Harris, Bernard; Roseberry Lincoln, Ann M.;
APPLICANT: Gerstin, Jr., Edward H.; Peralta, Careyna H.;
                                                                                                                            SOFTWARE: PERL Program
SEQ ID NO 150
LENGTH: 772
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                                                                                                                                                                                            Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/US01/27628
PRIOR FILING DATE: 2001-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/363,829
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                                                                                                            TYPE: DNA
                                                                                     ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                          FILING DATE: 2000-09-06
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                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/230,597
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/230,517
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/229,748
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                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/230,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/229,747
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Toman, Rebekah R.
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Pred. No. 24
                         LG:994938.1:2000SEP08
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US-10-363-829-237/c
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                                                                          US-10-363-829-237
                                                                                                                                                                  SOFTWARE: PER
SEQ ID NO 237
LENGTH: 810
TYPE: DNA
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Matches
                Query Match
Best Local Similarity
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APPLICANT:
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PRIOR FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: US 60/229,751
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 60/229,749
PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 60/229,750
DELIC STILL CATTON NUMBER: US 60/229,750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: MOLECULES FOR DISEASE FILE REFERENCE: PT-1183 USN
CURRENT APPLICATION NUMBER: US/10/363,829
CURRENT FILING DATE: 2003-03-05
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PRIOR
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                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-09-06 PRIOR APPLICATION NUMBER: US
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                                                                                          NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: LI:814261.1:2000SEP08
                                                                                                                                                  ORGANISM: Homo
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/230,597
                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 2000-09-05
APPLICATION NUMBER: US 60/230,583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US FILING DATE: 2000-09-05
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/230,517
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                                                                                                                                                                                                                            PERL Program
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Chalus, Michael S.; Jackson, Jennifer L.;
Jones, Anissa L.; Yu, Jimmy Y.;
Wright, Rachel J. Cirran
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Harris, Bernard; Roseberry Lincoln, An
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Conservative
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L, Christopher R.; Momiyama, Monika G.;
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                  22.3%;
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0; Mismatches
                    Score 31;
Pred. No.
  Mismatches
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                                  DB 19; Length 810;
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  Indels
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45 TTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCCAAAGCACC 104

Query Match

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; ORGANISM: Rattus norvegicus
US-10-486-706-223
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US-10-486-706-223/c
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             APPLICANT: SENOH, AKINIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, MASATO
APPLICANT: OZAKI, MASATO
APPLICANT: OZAKI, MASATO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
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SEQ ID NO 223
LENGTH: 2337
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CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION UNUMBER: US/0/311,343
PRIOR FILING DATE: 2001-08-13
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APPLICANT:
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NUMBER OF SEQ ID NOS:
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Similarity 56.3%;
58; Conservative
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YOKOI, HARUHIKO
TATEISHI, NAOKO
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Pred. No. 11;
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US-10-737-082-4/c
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FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
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Matches
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SEQ ID NO 2992
LENGTH: 2799
Sequence 4, Application US/10737082
Publication No. US20050130170A1
GENERAL INFORMATION:
APPLICANT: Bayer Healthcare LLC
APPLICANT: Beard, Chris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
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TYPE: DNA
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                                                                                                                                                                            2899996 ATCATCGÁCAGTGTCTGTTCÁCÁCCACCAAATTCÁCCGATCCÁACGTGATGÁTCGGT 2899940
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OCHIAI, KEIKO
YOKOI, HARUHIKO
TATBISHI, NAOKO
SENOH, AKIHIRO
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53.8%;
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Pred. No. 16
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RESULT 12
US-09-960-870-13/c
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Best Local S
Matches 64
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CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: US 10/737,082
PRIOR FILING DATE: 2003-12-16
NUMBER OF SEQ ID NOS: 300
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
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Best Local Similarity
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SEQ ID NO 4
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TITLE OF INVENTION: Identification and Verification of Methylation Marker Sequences
FILE REFERENCE: 1657/2032
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 10/737,082 PRIOR FILING DATE: 2003-12-16 NUMBER OF SEQ ID NOS: 300
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                                                                                76 GTTTATTAACTGTTTATCCCCAAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAA 135
                                                                                                                                                                                               l Similarity 53.
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Gannon, Allison
Harvey, Jeanne
Lechner, John F.
                                                                 Li, Zheng
VENTION: Identification and Verification of Methylation Marker Sequences
NCE: 1657/2035
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Lechner, John F.
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Gannon, Allison
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53.3%;
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Pred. No. 40;
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US-10-251-668-13/c
Sequence 13, Application US/10251668
Publication No. US20040063097A1
GENERAL INFORMATION:
APPLICANT: Evans, Glen
TITLE OF INVENTION: USE
TITLE OF INVENTION: USE
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; TYPE: DNA
; ORGANISM: M. genitalium
US-09-960-858-13
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Publication No. US20030134281A1
GENERAL INFORMATION:
APPLICANT: Evans, Glen
TITLE OF INVENTION: NANOMACHINE COMPOSITIONS AND METHODS
TITLE OF INVENTION: USB
TITLE REFERENCE: P-EA 4738
CURRENT APPLICATION NUMBER: US/09/960,870
CURRENT FILING DATE: 2001-09-20
NUMBER OF SEQ ID NOS: 19
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APPLICANT: Evans, G
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Matches
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SEQ ID NO 13
LENGTH: 31241
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CURRENT APPLICATION NUMBER: US/09/960,858
CURRENT FILING DATE: 2001-09-20
NUMBER OF SEQ ID NOS: 19
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FILE REFERENCE: P-EA 5441
CURRENT APPLICATION NUMBER: US/1
CURRENT FILING DATE: 2002-09-20
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nes 58; Conserv
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Pred. No. 53;
0; Mismatches
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Pred. No. 53;
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// TYPE: DNA
// ORGANISM: M. genitalium
US-10-251-668-13

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PRIOR FILING DATE: 2001-09-20
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FBSTSEQ for Windows Version 4
SEQ ID NO 13
SEQ ID NO 13
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Best Local Similarity 55.8%;
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LENGTH: 104644
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APPLICANT: Liang, Yinghua
TITLE OF INVENTION: Identification of Novel Gene Family Members Expressed by
TITLE OF INVENTION: Hematopoietic Cells
FILE REFERENCE: 180/132 PCT/US
CURRENT APPLICATION NUMBER: US/10/433,287
CURRENT FILING DATE: 2003-11-12
NUMBER OF SEQ ID NOS: 81
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NAME/KEY: Genomic DNA
LOCATION: (1)...(104644)
OTHER INFORMATION: n is an undetermined nucleotide (date, dcte, dgte, or dtte)
                                                                  NAME/KEY: misc_feature
LOCATION: (231)...(231)
OTHER INFORMATION: n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: homo sapiens
NAME/KEY: misc feature
LOCATION: (242)...(242)
OTHER INFORMATION: n is a,
                                                                                                                                                         NAME/KEY: misc feature LOCATION: (143)..(143)
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OTHER INFORMATION: n is
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LOCATION: (39)..(39)
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LOCATION: (1)..(3)
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; NAME/KEY: misc_feature; LOCATION: (104525); OTHER INFORMATION: n is a, c, US-10-433-287-79
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NAME/KEY: misc feature
LOCATION: (362)..(362)
OTHER INFORMATION: n i
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LOCATION: (11699)..(11699)
OTHER_INFORMATION: n is a, c,
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LOCATION: (11659)..(11659)
OTHER INFORMATION: n is a,
                                                                             NAME/KEY: MS4A12_coding_region LOCATION: (101182)..(101283)
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LOCATION: (32640)...(32640)
OTHER INFORMATION: n is a, c, g,
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NAME/KEY: MS4A7 initial coding_region
LOCATION: (17493)..(17639)
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| (cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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| (cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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	Sequence 205, App	Sequence 205, App		Sequence 11, Appl	Sequence 11, Appl	Sequence 148425,	Sequence 148424,	Sequence 40626, A	Sequence 40625, A	Sequence 113, App	•	Sequence 113, App	Sequence 113, App	•	Sequence 47920, A	Sequence 15654, A	Sequence 15393, A	Sequence 71, Appl

ALIGNMENTS

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US-09-949-016-16498/c
; Sequence 16498, Application US/09949016
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; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN G
; TITLE OF INVENTION: WITH HUMAN DISEASE, MET
; FILE REPERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; SOFTWARE: FASTSEQ for Windows Version 4.
; SEQ ID NO 16498
; LENGTH: 52494
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(52494)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16498
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
Sequence 15273, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE
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    J. Craig et al.
    POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

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; LOCATION: (1)...(102304)
; OTHER INFORMATION: n = A,T,C
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
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6000 ATTAAGTAACTATTGACAGAGCAGGAGTATC 5970
                                                                                     6060 TITAGCAACTCCAACATCATCCTCTCTCTTGCCAAGAAATTATATAAATATTTGTCATCTTG 6001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 AATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTTATT 82
                                         80 ATTAACTGTTTATCCCCAAAGCACCATAATC 110
                                                                                                                          20 TTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTTGTCTGGTTT 79
                                                                                                                                                                           54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATTGTTAACACA 139
                                                                                                                                                                             Conservative
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54.7%;
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                                                                                                                                                                             0; Mismatches 37;
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Pred. No. 1.6;
                                                                                                                                                                                                Score 31.8;
Pred. No. 2
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                                                                                                                                                                                                                    4; Length 102304;
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OF DETECTION AND USES THEREOF
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RESULT 4

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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08
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US-09-949-016-144837/c
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PRIOR FILING DATE: 2000-10-20
PRIOR PELICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
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Sequence 81832, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 81832
LENGTH: 601
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Best Local Similarity
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CURRENT FILING DATE: 2000-04-14
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                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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Local Similarity 54.5%;
                                                                                                  154 GAGACTTTGGGCAAATCACTTAATCTGTCTGTGCCTCAGTTTCCTTATCTATAAAATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60;
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                                                                                                                                                                                                    60;
94 GAGAATAATGGTGTCAACTTTTACTTTATAAAGATTAAATAAGATAGTC
                                              GTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATC 110
                                                                                                                                                GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG
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Pred. No. 1
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Pred. No. 1.
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US-09-949-016-15840
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US-09-949-016-14121
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
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Patent No. 6812339
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                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14121
LENGTH: 22823
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Best Local
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
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  3243 GAGACTTTGGGCAAATCACTTAATCTGTCTGTGCCTCAGTTTCCTTATCTATAAAATGGG
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                                    1. GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG 60
                                                                                           60; Conservative
                                                                                                                 Similarity
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                                                                                      Score 30; DB 4;
Pred. No. 5.3;
0; Mismatches 5
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ACPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILLE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FASTSEQ for Windows Variation 10 Nos 293
LENGTON
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US-09-949-016-15770, Application US/09949016
Sequence 15770, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
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US-09-949-016-15770
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US-09-439-313-293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6329505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 293,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                TYPE: DNA ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                                             Jiang Yuqui
Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                         Harlocker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09439313
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Pred. No. 14;
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Query Match

21.4%;

Score 29.8;

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Length 301;

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RESULT 10
US-09-352-616A-293
; Sequence 293, Application US/09352616A
; Patent No. 6395278
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                                                                 ; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 293
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-293
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; ORGANISM: Homo sapien
US-09-352-616A-293
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SEQ ID NO 293
LENGTH: 301
Query Match
Best Local S
Matches 55
                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C6
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
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Best Local Similarity
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APPLICANT:
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APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C8
CURRENT FILING DATE: 1999-07-13
RUMBER OF SEQ ID NOS. 472
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 Local Similarity 56.
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Pred. No. 0.98;
0; Mismatches 42;
Score 29.8; DB Pred. No. 0.98; O; Mismatches
                                DB 3; Length 301;
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SOFTWARE: FE
SEQ ID NO 293
LENGTH: 301
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Best Local Similarity
Matches 55; Conserv
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GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.428C5
                                               APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
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CURRENT FILING DATE: 1998-09-23
NUMBER OF SEQ ID NOS: 306
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                  Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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                                 FastSEQ for Windows Version 3.0
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Carter, Darrick
                                                                                                                                                                                                                                                                                                                                         Kalos, Michael D.
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Mitcham, Jennifer L.
                                                                                                                                                                                             Wang, Aijun
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                                                                                                                                                                                                               Li, Samuel
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Pred. No. 0.98;
0; Mismatches
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RESULT 14
US-09-685-166A-293
; Sequence 293, Application US/09685166A
; Patent No. 6630305
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                                                         RESULT 15
US-09-688-489-293
; Sequence 293, Application US/09688489
; Patent No. 6664377
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CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 293
LENGTH: 301
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Best Local Similarity
Matches 55; Conserv
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Best Local Similarity
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
 APPLICANT:
APPLICANT:
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer Lynn
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Carter, Darrick
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Kalos, Michael
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; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHE; TITLE OF INVENTION: CANCER AND METHODS FOR FILE REFERENCE: 210121.427D2; CURRENT APPLICATION NUMBER: US/09/688,489; CURRENT FILING DATE: 2000-10-13; NUMBER OF SEQ ID NOS: 338; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 293; LENGTH: 301
Search completed: August
Job time : 107 secs
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US-09-688-489-293
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ALIGNMENTS

Query Match 100.0%; Score 139; DB 6; Best Local Similarity 100.0%; Pred. No. 7.3e-29; Matches 139; Conservative 0; Mismatches 0; 121 121 TGTTCTTATTGTTAACACA 139 61 GTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGAC 13 Salmonella typhimurium Salmonella typhimurium Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella. Titball,R.W. and Bullifent,H.L. Recombinant microorganisms Patent: WO 0119974.A 2 22-MAR-2001; The Secretary of State for Defence Location/Qualifiers 1 GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG 1 GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG Sequence 2 from Patent WO0119974. AX100259.1 AX100259 GTGACTATTTGTCTGGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGAC TGTTCTTATTGTTAACACA 139 /organism="Salmonella typhimurium" /mol_type="unassigned DNA" /db_xref="taxon:602" GI:13539143 å DNA ଞ Length 139; Indels linear PAT 02-APR-2001 0 120 60 120 60 0

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F.Heffron,
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1 (bases 1 to 990)
Groisman, E.A., Chiao, E., Lipps,
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phoP gene; virulence protein.
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Salmonella typhimurium phoP virulence gene is a transcriptional
Cano, D.A., Martinez-Moya, M., Pucciarelli, M.G., Casadesus, J. and Garcia-Del Portillo, F.
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Bacteria; Proteobacteria; Gammaproteobacteria;
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LPDIAIVDLGLPDEDGLSLIRRWRSSDVSLPVLVLTAREGWQDKVEVLSSGADDYVTK
PFHIEEVMARWQALMRRNSGLASQVINIPPFQVDLSRRELSVNEEVIKLTAFEYTIME
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/protein_id="AAA27187.1"
/db_xref="GI:154264"
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/mol_type="genomic DNA"
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strain SL1344.
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AUTHORS
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Submitted (16-FEB-2000) Garcia-del Portillo C.S.I.C.-Universidad Autonoma de Madrid, Cer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 2459)
Garcia-del Portillo, F.
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                                                                                                                                                                                    GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCCTCTTTTCTTCAGAAAGAGG
TGTTCTTATTGTTAACACA 139
                                                                                                    GTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAAGCACCATAATCAACGCTAGAC
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                                                                                                                                                       GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG
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                                                                                                                                                                                                                                                       Conservative
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note="member of a two-component res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           function="virulence transcriptional regulator"
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                                                                                                                                                                                                                                                                              Score 139; DB 1;
Pred. No. 4.5e-29;
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~hlanco, 28049 Madrid,
                                                                                                                                                                                                                                                                                                         Length 2459;
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REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 4 AL627269/c LOCUS REFERENCE COMMENT DEFINITION FEATURES JOURNAL MEDLINE AUTHORS TITLE JOURNAL PUBMED gene AL627269 bp. Salmonella enterica serovar Typhi complete chromosome; segment 5/20. AL627269 AL513382 AL627269.1 GI:16502231 Hinxton, E-mail: F 1 (bases 1 to 254050)

Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D., Wain, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T.G., Sebaihia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T., Sebaihia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T., Connerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N., Farrar, T., Feltwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S., Jagels, K., Krogh, A., Larzen, T.S., Leather, S., Moule, S., O'Gaora, P., Parry, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G.
Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18
Nature 413 (6858), 848-852 (2001) Salmonella enterica subsp. enterica serovar Typhi Salmonella enterica subsp. enterica serovar Typhi Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; sequencing team, Sanger Centre, Hinxton, Cambridge CB10 1SA, UK Enterobacteriaceae; Salmonella. Details of S. typhi sequencing at the on the World Wide Web. Submitted (25-OCT-2001) Direct Submission Parkhill, 11677608 21534947 (bases 1 to 254050) http://www.sanger.ac.uk/Projects/S_typhi/). parkhill@sanger.ac.uk /organism="Salmonella enterica subsp. enterica serovar /mol_type="genomic DNA" /strain="CT18" ocation/Qualifiers db_xref="taxon:90370" Submitted on behalf of the Salmonalla Centre, Wellcome Trust Genome Campus, (Salmonella typhi) strain CT18, Sanger Centre BCT 04-JUL-2003 are available

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Sd

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gene

SGD

misc_feature

misc_feature

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gene

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Query Match
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Matches 136; Conserv
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                                                                                                                          GTGACTCTGGTCGACGAACTTAAATAATGCCTGCTCACCCTCTTTTCTTCAGAAAGAGG
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                                                                                                  GTGAATCTGGTCGACGAACTTAAATAATGTGTGCCTCACCCTCTTTTCTTCAGAAAGAGG
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                                                                                                                                                                                                                                                                                                       overlap
                                                                                                                                                                                                                                                                                                                         526 aa overlap
Fasta hit to YJJK_ECOLI (554 aa),
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                                                                                                                                                                                                                                                                                                                                                                                 note="Fasta hit to YBIT_ECOLI (530 aa),
                                                                                                                                                                                                                            96.5%;
97.8%;
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                                                                                                                                                                                                                            Score 134.2; DB 1
Pred. No. 4.7e-28;
                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                    DB 1;
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AE016839 AE014613
AE016839.1 GI:29137536
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Deng, W., Liou, S.-R., Plunkett, G. III, Mayhew, G.F., Rose, D.J.,
Burland, V., Kodoyianni, V., Schwartz, D.C. and Blattner, F.R.
Direct Submission
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Salmonella enterica subsp. enterica serovar Typhi Ty2
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.

1 (bases 1 to 300029)
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                                                                                                                                                                                                 /locus_tag="t1460"
/note="corresponds to STY1521
Salmonella typhi CT18"
                                                                                                                                                                                                                                                                                                                                                                   /traiblation="mmikkskamlplapalpsyamaaqacttlaiqdkogdiphortlb
ymqdlpsmltyypagtopdkktpdosogisyoakypplaitstidodsrdilsgmns
aglsssamminnaqlpplpassykqaipdsegmalarpatvgsvkqaikskepsp
elhregdblkspphyarydkkogsivusvenokerhyudnptrvmtngpappmhltnuln
ytqltmvdrssgtlggikvmqpdsgiaiadlpssdtsvsrpirgvyttyapqatsah
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wiviqsgngvivsdkkhlasdytieeilstrelvdshcarlaaqndnvdvinqieaiy
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/note="corresponds to STY1522 from
Salmonella typhi CT18"
                                                                                                                                                                                                                                                                                                                          1382.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="putative secreted hydrolase"
/protein_id="AAO69099.1"
/db_xref="GI:29137537"
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/sub_species="enterica"
/db_xref="taxon:209261"
HRMDQAINDNNVHGFYSLDKEFHLAISEASRNRVLFDMSRMLWEQRINIPYAGLDEQ9
                                                                                  /product="putative regulatory protein"
/protein_id="AAO69100.1"
/db_xref="GI:29137538"
                                                                                                                                                                                                                                                                                                                                                YNDINYKTWSLSQFKNATAPVFEKINVKG"
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|382. .2173
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/transl_table=11
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strain="Ty2"
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/transl_table=11
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72, section 6 of
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EMGMIFSAFFIGYALFNFIDGWASDKVGPKTVFLIAALLWSVEGLYGLVTGLWTMLI
EWGMIFSAFFIGYALFNFIDGWASDKVGPKTVFLIAALLWSVEGLYGLVTGLLATSL
GWRPAFGIIFLEGLVWYLLMYFIVSDKPTMSKRLAFEERIDFENHEDVILSDDGRATF
SLGYYMKQPMVWATTLAFFSYNYILFFFLTWFPSYLNHSLHLDIKEISIATVIFWVIG
AIGMVLGGVCSDVIYRITGNALLSRRLILGVCLAGAAVCVAVSGTVSTIGSAITLMSV
SLFLLYLTGFIYWAVIQDVVHKDKVGSVGGAMHGLANISGIIGPLVTGFIVQFSGKYD
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VIDAIKNITHGTMAQVVIEASGANSAIRNTLDLASFAGRISFTGWPKQETSLPTNLIT
YKELDLRGSRTSAGEFDEALRMLSTLEINPQDVVSKVVNLDEIFDAVKELDRYPERYL
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afrgtnplvtypriighevtgivloegtgmpdnikkgdrvivdpyiycghcypcsvgr
tnccenlnvigvhidgamoevythpahlihkipdnvpsemaplaepltialhalhran
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Salmonella typhi CT18"
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/locus_tag="t1461"
                                                                                                                                                                                                                                                            complement (6321. .7562)
/locus_tag="t1464"
/note="corresponds to STY1517 from Accession AL513382:
Salmonella typhi CT18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HNNIFFCRNSFECDLSHVLPDYREQISGTPLKYTLISTAPLAQVVRHYELLSQHWSF
DDMVTPAQWRHNUDIYIPTAKEHHALVVNNNGINYEKGIQIESKPVDFTQQTLASIA
RDTWTTPAQWRHNUDIYIPTQDDKYCDLKEDESYGRSWALFUBAFEQRELMPLAIFHYD
ROTROTIVISWSDIRQYLTFQDDKYCDLKEDESYGRSWALFUBAFEQRELMPLAIFHYD
AISQAMRLAKKELTQWNINSFIITGISKRGWTTWLSAIADDVEAIVPFAIDLLDIDA
SLEHIYGSYGGNWFITFYYSKLGOTOEKIKSPTTQLKQIIDDAEGSLVPFINRFQS
KYIINASGDDFVDNUTRFYYSKLGOTOEKIKSPTTQLKQIIDPAEGSLVPFINRFQS
KYIINASGDDFVDNUTRFYYSKLGOTOEKIKSPTTQLKQIIRQQDLTIDIPAN
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Salmonella typhi CT18"
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complement (4695. .6251)
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/protein_id="AAO69102.1"
/db_xref="GI:29137540"
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/protein_id="AAO69101.1"
/db_xref="GI:29137539"
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/transl_table=11
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complement / ^ ^ ^ *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /producT="hypothetical protein"
/protein id="AA069103.1"
/db xref="61:29137541"
/translation="MPKRYLWKLCWLAPALVKRGESMKKIYLVVIVLFFISTKVYTLL
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/transl_table=11
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/transl_table=11
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61

250247

GTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCCAAAGCACCATAATCAACGCTAGAC 250306 GTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGAC GTGAATCTGGTCGACGAACTTAAATAATGTGTGCCTCACCCTCTTTTCTTCAGAAAGAGG GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG

120

片 S

250187

Query Match Best Local Matches

136;

Conservative

0

Mismatches No. 4.5e-28;

Indels

<u>,,</u>

Gaps

0

60 250246

Similarity

96.5%; 97.8%;

Score 134.2; Pred.

DB 1;

Length 300029;

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gene
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                                                                                                                                                    /codon_start=1
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GVSGWLSRISLGAPIYAAFILVLGAALLVAIWGLEDFSTERTIGLIASGILKMF
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MLSNRKIQTKCVEEVTINEEYYEVPQATTADIINTAKQNGGRIPGREETTTRUSINANAY
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Salmonella typhi CT18"
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complement (11372. .12544)
/locus_tag="t1468"
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Salmonella typhi CT18"
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9429. .10508
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Salmonella typhi CT18"
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/note="corresponds to STY1515 from Accession AL513382:
NFNNI EKEVWVYDTDLKSFTTREVDLLDYDLPSAIGTLLGKVEGAI YAQRSTQLSATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transl_table=11
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/transl_table=11
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7.1"
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RESULT 6
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Best Local Sim:
Matches 129;
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TITLE
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Salmonella typhimurium
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae; Salmonella.

1 (bases 1 to 2190)
Miller,S.I., Kukral,A.M. and Mekalanos,J.J.
A two-component regulatory system (phoP phoQ) controls Salmonella
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S.typhimurium phoP protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Original source text: S.typhimurium (strain LT2) DNA. Draft entry and printed copy of sequence for [1] kindly provided by S.I. Miller, 01-MAY-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane protein;
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                                                                                                                                               TCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGGTGACTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGTTCTTATTGTTAACACA 139
                                                                     GTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAACGCTAGACTGTTCTTATT 130
                                                                                                                     TCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGGGTGACTATTT
                                                                                                                                                                                                                    Conservative
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PPHIEEVMARWQALMRRNSGLASQVINIPPFQVDLSRRELSVUSCVAUNTTWNDOG
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/db_xref="taxon:602"
141. .815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           815. .2170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLIRNNGKVVSKDSLMLQLYPDABLRESHTIDVLMGRLRKKIQAQYPHDVITTVRGQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="membrane protein pho0"
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                                                                                                                                                                                                                                        92.8%;
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                                                                                                                                                                                                                                           Score 129;
Pred. No.
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and membrane protein phoQ genes
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                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                               Length 2190;
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ORGANISM
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AE008754/c
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Submitted (29-MAR-2001) Genome Sequencing Center, Department of Genetics, Washington University School of Medicine, 4444 Forest Park Boulevard, St. Louis, MO 63108, USA
COMMENT Supported by NIH grant 5U 01 A143283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmonella typhimurium LT2
Salmonella typhimurium LT2
Bacteria, Proteobacteria; Gammaproteobacteria, Enterobacteriale
Bacteria, Proteobacteria; Gammaproteobacteria, Enterobacteriale
Bacteriaceae; Salmonella.

1 (bases 1 to 24578)
MCClellandd, M., Sanderson, K.E., Spieth, J., Clifton, S.W.,
Latreille, P., Courtney, L., Porwollik, S., Ali, J., Dante, M., Latreille, P., Courtney, L., Porwollik, S., Ali, J., Dante, M., Latreille, P., Courtney, L., Porwollik, S., Layman, D., Leonard, S., Nguyen, C., Scott, K., Holmes, A.,
Grewal, N., Mulvaney, E., Ryan, E., Sun, H., Florea, L., Miller, W.,
Stoneking, T., Nhan, M., Waterston, R., and Wilson, R.K.
                                                                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GLIMMER; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE008754 AE006468
AE008754.1 GI:16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg/, and Pedro Romero and Peter Karp at EcoCyc; http://ecocyc.PangeaSystems.com/ecocyc/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Salmonella typhimurium Genome Sequencing Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21534948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ReguonDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-Vides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EC numbers were kindly provided by Junko Yabuzaki and the Kyoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTAACACA 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 24578)
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/EC_number="
                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
note="similar to E. coli adenylosuccinate lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (888),
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                       number="4.3.2.2"
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gene

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complement(1,467...1472)
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AAYPEVUWHOPSEEFVTSLGIONNEYTTOIEPHDYLAELFDCIARPRITILIDEDDDVW
GYIALNHFKOKTIAGEIGSSTWPHKWEIDERBREGNLGLSNAVILHLLAKLEVSRWO
RDLTDSTVLRNLGVGIGYALIAYQSTLKGV$KLEVNRDHLLDELDHNWEVLAEPIQTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKLAAHAAI KEVPAFAADANGYLDTLVANFNEEDAARI KTI ERTTNHDVKAVEYFLKE
KVAAI PALHDVSEFIHFACTSED INNLSHALMLKTARDEVI LPYWRQVINAVKDLATQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (1461. .2108)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (1461. .2160)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="putative -10 signal RegulonDB:STMLTH004479"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRRYGIEKPYEKLKELTRGKRVDAEGMKQFIDSLALPEAEKTRLKAMTPANYIGRAVT
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complement(2189. .3340)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (2189. .3349)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="putative -35_signal RegulonDB:STMLTH004479"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (2152. .2160)
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complement(2112. .2117)
/note="putative RBS for trmU; complement(3349. .3820)
                                                                complement (3344. .3349)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to B. coli orf, hypothetical protein (AAC74216.1); Blastp hit to AAC74216.1 (213 aa), 94% jeentity in aa 1 - 213"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="ycfC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="synonym: STM1233"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="ycfc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MELSSLTAVSPVDGRYGDKVSALRGIFSEYGLLKFRVQVEVRWL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein_id="AAL20161.1"
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                                                                                                                                                                                                                                                                                                                                                                                  /EC number="2.1.1.61"
/note="similar to E. coli orf, hypothetical protein
(AAC74217.1); Blastp hit to AAC74217.1 (383 aa), 94%
identity in aa 1 - 383"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="ycfC"
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                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="ycfC"
                                        gene="trmU"
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                                                                                                                                                                                                                                                                                                                        product="tRNA
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                     RegulonDB:STMS1H001490'
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Best Local S
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                                                                                                                                                                                                                                                                                                ·35_signal
                                                                                             113
    53
                                             61 GTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCCAAAGCACCATAATCAAC 113
                                                                                                                                                                                                               Similarity
    GTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAAC
                                                                                               GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG
                                                                                                                                     GTGACTCTGGTCGACGAACTTAAATAATGCCTGCCTCACCCTCTTTTCTTCAGAAAGAGG
                                                                                                                                                                                          Conservative
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COMplement(3349. .3810)
/Gene-".mfr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MFKPHVTVACIVHAEDKFLVVEETINGKSLWNQPAGHLBADETL
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                                                                                                                                                                                                                                                                                                   /note="synonym: 4829. .4837
                                                                                                                                                                                                                                                                                                                                                                                                                      /note="putative binding STMS1H000184"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4740. .4754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (4154. .4159)
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synthase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="similar to B. coli orf, hypothetical protein (AAC74219.1); Blastp hit to AAC74219.1 (207 aa), 831 identity in aa 1 - 205"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (4148. .4813)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (4148. .4813)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="putative RBS for complement (3822. .4159)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (3815. .3820)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DHIDKPL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'gene="ymfB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene="ymfB"
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                                                                                                                                                                                                                                                                                                                                                                        /bound_moiety="FruR"
1829. .6235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="putative RBS for STM1236; RegulonDB:STMS1H001492"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="ymfC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="GI:16419754"
                                                                                                                                                                                                                                                                                /gene="icdA"
                                                                                                                                                                                                                                                                                                                                                   gene="icdA"
                                                                                                                                                                                                             81.3%;
100.0%;
                                                                                                                                                                                          0
                                                                                                                                                                                                             Score 113; DB 1;
Pred. No. 7.3e-22;
                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                  STM1238"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                site for FruR, RegulonDB:
                                                                                                                                                                                                                                  Length 24578;
                                                                                                                                                                                          Indels
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RBS

-10_signal

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RBS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AE008753/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                      gene
                                                                                 Sg
                                                                                                                                                          RBS
                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McClelland,M., Sanderson,K.E., Spieth,J., Clifton,S.W.,
Latreille,P., Courcney,L., Porwollik,S., Ali,J., Dante,M., Du,F.,
Hou,S., Layman,D., Leonard,S., Nguyen,C., Scott,K., Holmes,A.,
Grewal,N., Mulvaney,E., Ryan,B.4, Sun,H., Florea,L., Miller,W.,
Stoneking,T., Nhan,M., Waterston,R. and Wilson,R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GLIMMER; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (29-MAR-2001) Genome Sequencing Center, Department of Genetics, Washington University School of Medicine, 4444 Forest Park Boulevard, St. Louis, MO 63108, USA COMMENT Supported by NIH grant 5U 01 A143283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella typhimurium LT2
Salmonella typhimurium LT2
Sacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AE008753 22182
Salmonella typhimurium LT2, s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg/, and pedro Romero and Peter Karp at EcoCyc; http://ecocyc.PangeaSystems.com/ecocyc/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AE008753.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-Vides and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Salmonella typhimurium Genome Sequencing Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 413 (6858), 852-856 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE008753 AE006468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submission
/note="similar to E. coli orf, hypothetical protein
(AAC74196.1); Blastp hit to AAC74196.1 (85 aa), 91%
                                              'gene="ycfR"
                                                                                                    'note="putative
                                                                                                                            /gene="ycfR"
                                                                                                                                                                                                        'gene="ycfR"
                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                          /mol_type="genomic_DNA"
/strain="LT2; SGSC 1412; ATCC 700720"
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                                                                                                                                                                                     'note="
                                                                                                                                                                                                                                                                                                                                                                                           organism="Salmonella typhimurium LT2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:16419731
                                                                                                                                                                                                                                                                                          _xref="taxon:99287"
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                                                                                                    RBS for ycfR; RegulonDB:STMS1H001474"
                                                                                                                                                                                     STM1214"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 bp DNA
section 57
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of 220 of the complete
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                                                                                                                            gene
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                                                   CDS
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RGULIVFVNYLMQRVCPHSYLLHGHALVMKKGGRLSFDALRAQLDSAGYRHVDQVWEHG
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PANTLVVNTGSLETSAERFQADTLARREINGUPMRETLFPBALMTRUDELFSESFLFRW
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GRREALGELLARIKARKFRILKLDEAQDAGRYLMMGAREHFIOTORNLALICESDIL
GERVARRRLDSRRTINPDTLIRNLAELHVQQPVHLBHGVGRYAAMTTLEAGGIKGEY
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LVCGDVGFGKTEVAMRAAFLAVENHKQVAVLVPTTLAQOHYDUFBDRFAMWPVAIEM
LSFFRSAKEQTQILTLFATPIFRTLANANSGMRDLSIIATPBARRLAUVKTFVRESYBSLVV
REAILREILRGGQVYYLYNDVENIQKAAERLAELVPBARIAIGHGAGELLGEEQGSGMETIGF
FHQRRWVLVCTTIIETGIDIFTANTIIETRADHFGLAQHQLRGRVGRSHHQAYAML
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ASAKUENELEEIKVELLDRFGLLDDFANILDIARKTRIDDWVRQFMQQLEENA
FABKNHVDPANILGILLQKQPQHFRLDGFTRLKFIQDLSBRKKTRIDWVRQFMQQLEENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GI:16419733"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="ycfS"
/note="putative RBS for ycfS;
complement(1617. .5081)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mknvktliaaavlsslsfasfaavevQatpegQQkfGTIsanGG
TNLGSLEDQLaQkaQemGakSfritsvTGFNTLHGTAVIYK"
                                                                                                                                                                    5290. .6600
                                                                                                                                                                                                                                                                      complement (5076.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor; mutation frequency decline (AAC74198.1); Bit
hit to AAC74198.1 (1148 aa), 95% identity in aa 1 -
/codon start=1
/transI_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (1617. .5063)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to E. coli orf, hypothetical
(AAC74197.1); Blastp hit to AAC74197.1 (320)
identity in am 1 - 320"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (504. .1469)
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/protein_id="AAL20143.1"
/db_xref="GI:16419732"
                                                           /note="synonym:
5290. .6600
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/protein_id="AAL20145.1"
/db_xref="GI:16419734"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/transI_table=11
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/protein_id="AAL20144.1"
/gene="ycfU"
/note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="similar to E. coli transcription-repair coupling actor; mutation frequency decline (AAC74198.1); Blastp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="mfd"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="synonym: STM1216"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="mfd"
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/transl_table=11
                                                                                                                             gene="ycfU"
                                                                                                                                                                                                   note="putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dentity in aa 1
                                                                                                                                                                                                   RBS
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                                                                                                                                                                                                                                                                      .5081)
E. coli orf, hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outer
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                                                                                                                                                                                                   for mfd;
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                                                                                                                                                                                                   RegulonDB:STMS1H001476"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RegulonDB:STMS1H001475"
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aa), 841
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gene

RBS

Sg

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Query Match
Best Local S
Matches 86
  22122
                                                                                                22182
                                                                                                                                              54
                                                                                                                                                                                              98
                                                                                                                                                                                                                     Similarity
                           GCTAGACTGTTCTTATTGTTAACACA
                                                                                                                       AAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCAAAGCACCATAATCAAC 113
GCTAGACTGTTCTTATTGTTAACACA
                                                                                             AAAGAGGGTGACTATTTGTCTGGTTTATTAACTGTTTATCCCCCAAAGCACCATAATCAAC 22123
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIGLRYMRGRAADRFGRFVSWLSTIGITLGVMALVTVLSVMNGFERELQNNILGLMPQ
ALLSAEHGSLMPNQMPEKAVNLQGVNRI AFLTTGDVVLQSARSVAVGVNLGIDPAQKD
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RLFTVIGTFAANSEVDGYEMLVNIQDASRLMRYPAGNITGWRLWLDBFLQVDTLSQQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="similar to E. coli putative ATP-binding component of a transport system (AAC74201.1); Blastp hit to AAC74201.1 (228 aa), 94% identity in aa 1 - 228"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="synonym: 6580. .6585
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GSGKSTLLHLLGGLDTPTSGDV1FSGQDMSKLSSAAKAELROQKLGFIYQFHLLDDF
TALENVAMPLIGKKKPAEIDARAFSIDARAFSHLAVGLEHRATHFSELSGGERQLTATAF
TALENVAMPLIGKKKPAEIDARAFSID FELLGELNRLQGTAFLVVTHDLQLAKRMSRQLEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon start=1
/transI_table=11
/product="integral membrane protein ABC transporter"
/protein id="AAL20148.1"
/db_xref="GI:16419737"
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/protein_id="AAL20147.1"
/db_xref="GI:16419736"
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/transl_table=11
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6593. .7294
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/db_xref="GI:16419735"
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7280. .7285
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Pred. No. 3.5e-14;
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02.1 (414 aa), 92% identity in aa 1
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On Jun 30,
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Bacteria; Proteobacteria;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 166554)
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                                                Submitted (10-JUL-2004) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                            Wilson, R.K.
Direct Submission
                                                                                                                Direct Submission
Submitted (30-JUN-2004) Genome
Parkway, St. Louis, MO 63108, U
                                                                                                                                                      Wilson, R.K.
                                                                                                                                                                   Parkway, St. Louis, MO
4 (bases 1 to 166554)
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                                                                                                                                                                                                                     Wilson, R.K.
                                                                                                                                                                                                                                 Parkway, St. Louis, MO
3 (bases 1 to 166554)
                                                                                                                                                                                                                                                            Submitted (11-FEB-2002)
                                                                                                                                                                                                                                                                                   2 (bases 1 to 166554)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                               The sequence of Mus musculus Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                          Nguyen,C., Meyer,R., Dignan,G., Creason,K., Haglund,K.
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Center: Washington University Genome Sequencing Center
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HEALTH INC (US); WASHINGTON UNIVERSITY
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:562"
                        2004 this sequence version replaced gi:47084610.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C5/BL/GJ mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEIGHBORING SEQUENCE INFORMATION: This sequence is the entire insert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
----- Summary Statistics
Center project name: M_BB0198116
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6772
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/db_xref="taxon:10090"
/chromosome="10"
   /rpt_family="Alu"
9107. .9257
                               /rpt_family="MER1_type"
9075._.9188
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9283. .9468
                     /rpt_fi
25565.
                                                   /rpt_family="ID"
25386. .25462
                                                                                                                                                /rpt_family="MaLR"
23635. .23898
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16734. .1670/
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12427. .1
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10691. .10832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="Sequence derived from one plasmid subclone."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="Unresolved tandem repeat."
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18 Galagan, J. E., Nusbaum, C., Roy, A., Endrizzi, M.G., Macdonald, P., Galagan, J. E., Calvo, S., Engels, R., Smirnov, S., Atnoor, D., Brown, A., Allen, N., Naylor, J., Stange-Thomann, N., DeArellano, K., Johnson, R., Linton, L., McEwan, P., McKernan, K., Talamas, J., Tirrell, A., Ye, W., Zimmer, A., Barber, R. D., Cann, I., Graham, D. E., Grahame, D. A., Zimmer, A., Hedderich, R., Ingram-Smith, C., Kuettner, C.H., Krzycki, J.A., Leigh, J.A., Li, W., Liu, J., Mukhopadhyay, B., Reeve, J.N., Smith, K., Springer, T. A., Umayam, L. A., White, O., White, R. H., Ge Macario, E. C., Ferry, J. G., Jarrell, K. F., Jing, H., Wacario, A. J. L., Paulsen, I., Pritchett, M., Sowers, K. R., Swanson, R. V., Zinder, S. H., Lander, E., Metcalf, W. W. and Birren, B. The Genome of M. acetivorans Reveals Extensive Metabolic and Physiological Diversity
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Direct Su
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanosarcina acetivorans C2A
Methanosarcina acetivorans C2A
Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AE010854 11716 bp Methanosarcina acetivorans str.
                                                                                                                                                                    Submitted (20-MAR-2002) Center for Genome Research, Wh. Institute, Nine Cambridge Center, Cambridge, MA 02141, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complete genome.
AE010854 AE010299
AE010854.1 GI:19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTCACGATGCCTGCATCATTCACCTCTCTCACTAAGACTGCATCATGATGCCT 100169
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28500.
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25953.
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/gene="MA1763"
complement (648. .1085)
/gene="MA1763"
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                                                          complement (648. .1085)
                                                                             /db_xref="taxon:188937"
                                                                                             'mol_type="genomic DNA"
'strain="C2A"
                                                                                                                                 organism="Methanosarcina acetivorans C2A
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Pred. No. 2.6;
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A, section 199 of 534 of the
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/db xref="id=
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/transl_table=11
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/db_xref="GI:19915655"
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SSITANTSCNIGATISNTGESDAGTFNATLSVWGAVVDTHAVSGIVSGSSATVNFSWK
PVAAGYYSVKVSADAGNVIAESDETNNELADCIKVEEASSGSQSQNGSSSSLAVTU
PVVCCFEVSPSALKFGELSAGQTSEPQLLTLKNCGVSGIKVTAEVSDSSAEDNLFGLGL
LLDSQIWSDYCNVIGSNSQENATAALHVPSDYTGTGNKKGTITFWAEVAE"
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LISYITYYBWMEDIKGRRVGTIAVIYDHKKSGLSNSIINVQHHYSHLIKYSVHMYLDT
DDCFELIVLDGNGQBITELAGSIIALKGVKFSKLTTVDPNKKI"
complement (2087. .4807)
TYTYTAVIDPDNLIAETDETNNIKSSSAKPLRYNGYKGKGIYMEGGSNITTMHTFDLO
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LNINPNGNTLDNGNISTGNGTLYRDMSNEGAYANYEYGLCVYDVTDKFSSAGNSLVMT
PVGBNKNALYPSTLVVVYGNDMETRKQIFINEECDELGLSASSYGTTPEERATAYAFFT
GISIDVEKVTNAMLYSFAGSAGPDEGNILFNGNIVATNAMQGSSNSGSPLAFDATNYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mokrsgylisillafatilsalictglaeaspsliiepseeisl
GTGEICELSLSADSLPEGLSGYKLTVELTDPDVAEIQAVNFPEWASLTDVSELPASSV
KLKAVDLQEAIDGEAEDVELAVLTLKGLEGGSTGITVTVSKMDDDSENTIILEGABYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (5861. .11104)
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/codon_start=1
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/gene="MA1765"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MA1766"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 44532)
Sulston, J.E. and Waterston, R.
                                                                                      Materacy, Materacy Direct Submission
Submitted (24-MAR-2002) Genome
Submitted (24-MAR-2002) Genome
Medicine,
                                                                                                                                                                                                                                   Direct Submission
Direct Submission
Submitted (14-MAR-2002) Genome Sequencing Center, Washington
Submitted (14-MAR-2002) Genome Sequencing Center, Washington
Submitted (14-MAR-2002) Genome Sequencing Center, Washington
                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (07-FBB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scott, K. and Haglund, K.
The sequence of Homo sapiens
Unpublished (2001)
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AC109830
AC109830.5 GI:19698745
                                                                                                                                                                          5 (bases 1 to 44532) Waterston, R.H.
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                       Waterston, R
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                                                                           63108, USA
                                               (bases 1 to 44532)
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PSVSEPDLLVSALTLNAGESFANEENTVGAKVERKGTANAGSFTVRFDVADISTRVSV
DGLSAGANITLSITDPSIRAYGDSVEITATTDTERSISIESNETNNALSITKTVVVNGY
KGKRWTDGDDINTRATFEGKYDIIYSGGDSVYTSSKWLSVTDTWTSSDLSIPADASVV
SARLYQPYSYNKMGIDPSFTAVENGATISTDATYKDIKGSYNEPYGLLVYNVTDQF
STAGNTLVLTPEGSAGTTNDYALMGAYLIVVYSDQETTEKQIFINDEFDMLYSKSSYS
VTSDEALAYANLSGUDYTEDIGSABVVSILASAGDSGKSKFFFNGEEYPGFWADAVHDDS
KIGFSVYNVTDGIASGANEARFQSYDAGTGGDNVYAMNAILVVEYSBSAFMADFMANT
TSGTAFLSVQFTDLSENATGWYNNFGDGANSTEQNFEITYSAGNYTVNLTVTNTAGS
DSEVKTDYIMYSBSSTPAFFIAMFTADVTGGTVPLTVNPTDQSAGSTSKFWDFDGOGA
NSTEQNPSHTYTSAGNYTVNLTVENAAGSDFELKSDYIEVSBAAFTSVTLFFDFENSS
VSENKETSISIVASNFFAGFSGYNMTVTLDPAVASIUTEYSBAAFTSVTLFFDFENSS
VSENESTEISIVASNFFAGFSGYNMTVTLDFAVASIUTEYSBAAFTSTLFFDFELTG
KIEVTLLSPLFDQGYAFREDLDGGGIYEDLTGNGEFSFVDVVAYFHMDWIEENMFVEY
FDFNGNGRIDFDDVVDMFAMI"
Submission
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VERSION KEYWORDS

DEFINITION

SOURCE

ORGANISM

REFERENCE

AUTHORS TITLE JOURNAL MEDLINE PUBMED

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Matches

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University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Mar 24, 2002 this sequence version replaced gi:19424675.
                                                                         USA
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COMMENT

Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu-Summary Statistics Center project name: H_NH1226B08 Center: Washington University Genome Sequencing Center Center code: WUGSC

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc Ö

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Freng Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either Research Genetics, Inc. (http://www.resgen.com) or Pieter de and coworkers at http://www.chori.org Frengen, E., Jong male from

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is AC015631, 2000 bp overlap;
clone sequenced to the right is RP11-400D2, 2000 bp overlap.
Actual end is at base position 85524 of RP11-400D2.
Location/Qualifiers

FEATURES repeat_region source repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region /rpt_family="L2" 697. ...731 /rpt_family="MIR" 5322. .5350 /rpt_family="ERVL" 2915. .3149 /rpt_family="AT_rich" 2447. .2850 /rpt_family="MIR" 3643. .4062 /rpt_family="(TCTA)n" 1428. .1478 /rpt_family="AT_rich" 1274. .1319 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="4" /clone="RP11-1226B8" /clone_lib="RPCI-11" rpt_family="MaLR" .44532 _family="AT_rich" family="MIR'

REFERENCE AUTHORS TITLE

Submitted (30-MAR-2002) Department of Genetics, Washington

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RRS MIZIN, D. MARTIE., MELEKER, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks, S., Amin, Baca, E., Baden, H., Baldaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Beiswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Barnstead, M., Benahmed, F., Burch, P., Dayla, K., Calderon, E., Calderon, E., Caderon, E., Davila, M., L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davis, C., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davis, C., Davis, C., Durbin, K., Duval, B., Eaves, K., Draper, H., Divya, K., Duval, B., Eaves, K., Draper, H., Divya, K., Duval, B., Eaves, K., Draper, H., Divya, K., Duval, B., Eaves, K., Eggan, A., Escotto, M., Eugene, C., Evans, C.A., Poster, P., Farser, C., K., Gall, R., Garcia, A., Garner, T., Garza, M., Gebrageorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gebrageorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gebrageorgis, B., Haedun, S., Hamelton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Jackson, A., Hogues, M., Hogues, M., Hernandez, J., Jang, H., Johnson, B., Johnson, R., 
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Rattus norvegicus clone CH230-171118, *** SEQUENCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC103069.5 GI:30579796
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31513. .31702
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70.6%;
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Pred. No. 4.8;
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HTG 13-MAY-2003 3 IN PROGRESS

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Gaps

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AL Submitted (13.MAY:2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:23268957.
On May 13, 2003 this sequence version replaced gi:23268957.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hggc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, B., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., A., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shety, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Sneed, A., Stong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Valas, R., Vera, V., Villasana, D., Waldron, L., Wanker, B., Wang, J., Wang, O., Wang, S., Warren, R., Wei, X., White, F., Wang, C., Wang, S., Warren, R., Wei, X., White, F., Willson, R., Wilson, R., Walker, B., Wang, V., V., Yu, F., Zhang, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                      * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 7 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: Estimated insert size may differ from sequence length
                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 245108)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.hgsc.bcm.tmc.edu/
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4120: contig of 4120 bp in length 4220: gap of unknown length 230259: contig of 226039 bp in length
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COMMENT

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AUTHORS TITLE

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TITLE JOURNAL REFERENCE

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SOURCE
ORGANISM
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Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks S., Amin, A., Anguiano, D., Allen, C., Allen, H., Alsbrooks S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Banyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Banyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Banyalebechi, V., Barnareead, M., Benahmed, F., Balyth, P., Barnareead, M., Benahmed, F., Barnareead, M., Bandaranaike, D., Barber, M., Barnareead, M., Benahmed, F., Biswalo, K., Blair, J., Barnaread, K., Center, M., Center, A., Canderon, M., Carden, M., Carden, M., Center, A., Center, A., Canderon, E., Chacko, J., Chavez, D., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chacko, J., Chen, G., Chen, R., Center, A., Center, A., Droband, C., Coyle, M., Cree, A., D'Souza, I., Davila, G., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Ceveland, C., Davy-Carroll, L., De Anda, C., Dederich, D., Davila, M., Lonson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Dayal, B., Eaves, K., Bagan, A., Bacter, A., Durbin, K., Duval, B., Eaves, K., Bagan, A., Bectto, M., Berrad, M., Berrad, M., Garrer, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Garza, M., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, K., Hernandez, S., Hulyk, S., Hume, J., Hernandez, J., Jackson, A., Jackson, A., Hodeson, A., Hogues, M., Hamilton, K., Hamilton, K., Hanyes, A., Henderson, N., Hernandez, J., Jackson, A., Jack
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
Rattus norvegicus
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/clone="CH230-171118"
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233662: contig of 3303 b
233762: gap of unknown 1
235430: contig of 1668 b
235430: gap of unknown 1
238472: contig of 2942 b
238572: gap of unknown 1
238572: gap of unknown 1
241059: contig of 2487 b
241159: gap of unknown 241159 gap of unknown 3
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64.6%;
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Submitted (20-NoV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:22856569.
On Nov 20, 2002 this sequencing reads assembled using Atlas the sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
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Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G., and Gibbs, R.A.
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3 (bases 1 to 162561)
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
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                                                                                                                                                                                                                                                                                                                                               Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Baylor College of Medicine Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.hgsc.bcm.tmc.edu/
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TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

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JOURNAL
REFERENCE
AUTHORS
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------ Genome Center
Center: Department Of Chemistry And Biochemistry
The University Of Oklahoma
                                                                                    The University Of Oklahoma,
                                                                                              Submitted (01-OCT-2004) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                     Lin,S., Dixon,R., May,G., Summer,L., and Roe,B.A.
                                                                                                                                                                                         OK 73019, USA
4 (bases 1 to 126477)
                                                                                                                                                                                                                         Submitted (28-SEP-2004) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                       Lin,S., Dixon,R., May,G., and Roe,B.A.
                                                                                                                                                                                                                                                                                                                                                            The University Of Oklahoma,
                                                                                                                                                                                                                                                                                                                                                                      Submitted (23-SBP-2003) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                              and Roe, B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Lin, S., Dixon, R., May, G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC146720.23
                                                        On Sep 28, 2004 this sequence version replaced gi:52694008
                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                    OK 73019, USA
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Pred. No. 5.7;
0; Mismatches
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                                                                                              Room 208, Norman,
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FEATURES

Location/Qualifiers

1. 126477

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/mol_type="genomic DNA"
/dbxref="taxon:3880"
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